



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174198

TO: Sumesh Kaushal
Location: REM-2B85/2C70
Art Unit: 1633
Friday, December 23, 2005
Case Serial Number: 10/787382

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Kaushal,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
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OM protein - protein search, using sw model

Run on: December 17, 2005, 07:25:38 ; Search time 46 Seconds
(without alignments)
26.959 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74

Sequence: 1 FAVENPMRLVAETL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5-COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6-COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H-COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/pCTrus COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	74	100.0	115	2	US-09-451-527-86
3	74	100.0	134	2	US-09-322-409-81
4	74	100.0	134	2	US-09-451-527-81
5	74	100.0	134	2	US-09-371-615A-2
6	43	58.1	69	2	US-09-248-796A-22862
7	39	52.7	559	2	US-09-543-681A-7241
8	38	51.4	341	2	US-09-902-540-13873
9	38	51.4	549	2	US-09-134-000C-4375
10	38	51.4	664	2	US-09-591-095-4
11	38	51.4	860	2	US-09-252-991A-26112
12	38	51.4	1205	2	US-09-252-991A-28876
13	37	50.0	133	2	US-09-371-615A-8
14	37	50.0	236	4	PCT-US91-08177-17
15	37	50.0	241	2	US-10-187-790A-16
16	37	50.0	557	2	US-09-949-002-347
17	37	50.0	578	2	US-09-949-002-428
18	37	50.0	586	2	US-08-459-953A-10
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22	36	48.6	196	2	US-09-328-352-4939
23	36	48.6	201	2	US-09-711-164-309
24	36	48.6	201	2	US-09-492-709A-391
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55	35	47.3	359	2	US-09-248-796A-17869	Sequence 17869, A
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57	35	47.3	447	2	US-09-583-110-4550	Sequence 4550, Ap
58	35	47.3	532	2	US-09-902-540-14357	Sequence 14357, A
59	35	47.3	2108	2	US-09-252-991A-31502	Sequence 31502, A
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62	34	45.9	67	1	US-08-484-101B-19	Sequence 19, Appl
63	34	45.9	67	1	US-08-714-524D-19	Sequence 19, Appl
64	34	45.9	110	2	US-09-270-767-62333	Sequence 62333, A
65	34	45.9	112	2	US-10-104-047-3840	Sequence 3840, Ap
66	34	45.9	127	2	US-09-855-323-12	Sequence 12, Appl
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77	34	45.9	159	2	US-09-303-518D-356	Sequence 356, App
78	34	45.9	159	2	US-09-303-518D-358	Sequence 358, App
79	34	45.9	159	2	US-09-303-518D-362	Sequence 362, App
80	34	45.9	159	2	US-09-303-518D-364	Sequence 364, App
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83	34	45.9	169	2	US-09-401-415-22	Sequence 22, Appl
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85	34	45.9	174	1	US-08-687-559-21	Sequence 21, Appl
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89	34	45.9	174	2	US-09-401-415-23	Sequence 23, Appl
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91	34	45.9	176	2	US-09-134-000C-4221	Sequence 4221, Ap
92	34	45.9	178	1	US-08-324-003A-25	Sequence 25, Appl
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94	34	45.9	179	1	US-08-687-559-24	Sequence 24, Appl
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101 34 45.9 214 2 US-09-248-796A-17961 Sequence 17961, A
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103 34 45.9 249 2 US-09-134-000C-5219 Sequence 5219, Ap
104 34 45.9 254 2 US-09-248-796A-24590 Sequence 24590, A
105 34 45.9 283 2 US-09-314-701-26 Sequence 26, Appl
106 34 45.9 283 2 US-10-314-639-26 Sequence 26, Appl
107 34 45.9 283 2 US-10-059-964A-26 Sequence 26, Appl
108 34 45.9 300 2 US-09-270-767-45716 Sequence 46716, A
109 34 45.9 326 2 US-09-252-991A-18289 Sequence 18289, A
110 34 45.9 345 2 US-09-107-532A-3849 Sequence 3849, Ap
111 34 45.9 349 2 US-09-252-991A-27933 Sequence 27933, A
112 34 45.9 354 1 US-08-843-530B-30 Sequence 30, Appl
113 34 45.9 354 2 US-09-636-728-27 Sequence 27, Appl
114 34 45.9 361 2 US-09-543-681A-7310 Sequence 7310, Ap
115 34 45.9 376 2 US-09-091-725-15 Sequence 15, Appl
116 34 45.9 391 2 US-09-543-681A-5945 Sequence 5945, Ap
117 34 45.9 488 2 US-09-489-039A-13363 Sequence 13363, A
118 34 45.9 494 2 US-09-252-991A-24309 Sequence 24309, A
119 34 45.9 512 2 US-09-107-532A-7248 Sequence 7248, Ap
120 34 45.9 528 2 US-09-543-681A-5551 Sequence 5551, Ap
121 34 45.9 551 2 US-09-252-991A-44209 Sequence 24209, A
122 34 45.9 591 2 US-09-252-991A-27090 Sequence 27090, A
123 34 45.9 641 2 US-09-270-767-44970 Sequence 44970, A
124 34 45.9 714 2 US-09-252-991A-24776 Sequence 24776, A
125 34 45.9 751 2 US-08-969-415-2 Sequence 2, Appli
126 34 45.9 751 2 US-09-538-092-127 Sequence 127, App
127 34 45.9 900 2 US-09-248-796A-18281 Sequence 18281, A
128 34 45.9 947 2 US-09-252-991A-29359 Sequence 29359, A
129 34 45.9 1096 2 US-09-792-024-120 Sequence 120, App
130 34 45.9 1218 2 US-09-252-991A-24869 Sequence 24869, A
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135 34 45.9 3144 2 US-08-556-419-21 Sequence 21, Appl
136 34 45.9 3144 2 US-09-041-886-15 Sequence 15, Appl
137 34 45.9 3144 2 US-09-538-092-1118 Sequence 1118, Ap
138 33 5 45.3 138 2 US-09-902-540-14591 Sequence 14591, A
139 33 44.6 36 2 US-09-057-363C-58 Sequence 58, Appl
140 33 44.6 43 2 US-09-265-107-58 Sequence 58, Appl
141 33 44.6 43 2 US-08-379-437-6 Sequence 6, Appli
142 33 44.6 57 1 US-09-492-709A-370 Sequence 370, App
143 33 44.6 103 2 US-08-893-534A-6 Sequence 6, Appli
144 33 44.6 108 2 US-08-996-673-6 Sequence 6, Appli
145 33 44.6 108 2 US-08-939-853A-8 Sequence 8, Appli
146 33 44.6 108 2 US-09-115-395-6 Sequence 6, Appli
147 33 44.6 108 2 US-09-113-977C-35 Sequence 35, Appli
148 33 44.6 108 2 US-09-507-102-6 Sequence 6, Appli
149 33 44.6 108 2 US-09-250-059-6 Sequence 6, Appli
150 33 44.6 108 2 US-09-250-059-6 Sequence 6, Appli
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ALIGNMENTS

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RESULT 1
US-09-322-409-86
; Sequence 86, Application US/09322409
; Patent No. 6471957
; ORGANISM: Canis familiaris
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0

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Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETL 15
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Db 1 FAVENPMRLVAETL 15
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RESULT 3
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; ORGANISM: Canis familiaris
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0

Query Match 100.0%; Score 74; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETL 15
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Db 1 FAVENPMRLVAETL 15
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Query Match 100.0%; Score 74; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15
Db 20 FAVENPMNRLVAETL 34

RESULT 4
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris

US-09-451-527-81

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Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15
Db 20 FAVENPMNRLVAETL 34

RESULT 5
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris

US-09-371-615A-2

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Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15
Db 20 FAVENPMNRLVAETL 34

RESULT 6
US-09-248-796A-22862
; Sequence 22862, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22862
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-22862

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Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAE 13
Db 25 IENPLNRLTAK 35

RESULT 7
US-09-543-681A-7241
; Sequence 7241, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7241
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Proteus mirabilis

US-09-543-681A-7241

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Best Local Similarity 42.9%; Pred. No. 79;
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Qy 1 FAVENPMNRLVAET 14
Db 397 FSLEKPNRLINT 410

RESULT 8
US-09-902-540-13873
; Sequence 13873, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiesand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13873
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13873

Query Match 51.4%; Score 38; DB 2; Length 341;
Best Local Similarity 63.6%; Pred. No. 67;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVENPMRLVA 12
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DB 26 AVQSPDLRLVA 36
| | | | |

RESULT 9
US-09-134-000C-4375
; Sequence 4375, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4375
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (73)..(73)
; OTHER INFORMATION: Amino acid 73 is Xaa whersin Xaa = any amino acid.
US-09-134-000C-4375

Query Match 51.4%; Score 38; DB 2; Length 549;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETL 15
| | | | |
DB 218 AVDMFQNSVEETL 231
| | | | |

RESULT 10
US-09-591-095-4
; Sequence 4, Application US/09591095
; Patent No. 6489461
; GENERAL INFORMATION:
; APPLICANT: Froman, B. & Dehesh, K.
; TITLE OF INVENTION: Nucleic Acid Sequences encoding Proteins
; TITLE OF INVENTION: Involved in Fatty Acid Beta-Oxidation and Methods of Use.
; FILE REFERENCE: 17137/01/US
; CURRENT APPLICATION NUMBER: US/09/591,095
; CURRENT FILING DATE: 2000-06-08
; EARLIER APPLICATION NUMBER: US 60/138,162
; EARLIER FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-591-095-4

Query Match 51.4%; Score 38; DB 2; Length 664;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
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QY 1 PAVENPMRLVAETL 15
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DB 32 FDSVNSRLVANDL 46
| | | | |

RESULT 11
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26112
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112

Query Match 51.4%; Score 38; DB 2; Length 860;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETL 15
| | | | |
DB 744 DNPVNLVAKGL 755
| | | | |

RESULT 12
US-09-252-991A-28876
; Sequence 28876, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28876
; LENGTH: 1205
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28876

Query Match 51.4%; Score 38; DB 2; Length 1205;
Best Local Similarity 61.5%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
| | | | |
DB 964 VDNRLRLQAETL 976
| | | | |

RESULT 13
US-09-371-615A-8

; Sequence 8, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:

; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: CANINE INTERLEUKIN 5
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8

; LENGTH: 133
; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:
; OTHER INFORMATION: Interleukin 5

US-09-371-615A-8

Query Match 50.0%; Score 37; DB 2; Length 133;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETL 15

Db 20 AMEIPMSTVVKETL 33

RESULT 14

PCT-US91-08177-17
; Sequence 17, Application PC/TUS9108177

; GENERAL INFORMATION:

; APPLICANT: Samal, Siba K

; TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., suite 1000
; CITY: Washington
; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/08177

; FILING DATE: 19911104

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/608,937

; FILING DATE: 05-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Hightet, David W

; REGISTRATION NUMBER: 30,265

; REFERENCE/DOCKET NUMBER: 20509-96711

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4854

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 236 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Bovine respiratory syncytial virus

; STRAIN: FS-1

PCT-US91-08177-17

Query Match 50.0%; Score 37; DB 4; Length 236;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ENPMNRLVAETL 15

Db 90 ENPTRLTKETI 101

RESULT 15

US-10-187-790A-16
; Sequence 16, Application US/10187790A

; Patent No. 6908618

; GENERAL INFORMATION:

; APPLICANT: SAMAL, SIBA K.

; TITLE OF INVENTION: PRODUCTION OF NOVEL BOVINE RESPIRATORY SYNCYTIAL

; FILE REFERENCE: 108172-00076

; CURRENT APPLICATION NUMBER: US/10/187,790A

; CURRENT FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 09/554,131

; PRIOR FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/23231

; PRIOR FILING DATE: 1998-11-09

; PRIOR APPLICATION NUMBER: 60/064,091

; PRIOR FILING DATE: 1997-11-10

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 16

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Bovine respiratory syncytial virus

US-10-187-790A-16

Query Match 50.0%; Score 37; DB 2; Length 241;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ENPMNRLVAETL 15

Db 95 ENPTRLTKETI 106

RESULT 16

US-09-949-002-347

; Sequence 347, Application US/09949002

; Patent No. 6900016

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,002

; CURRENT FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/231,401

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 347

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Human

US-09-949-002-347

Query Match 50.0%; Score 37; DB 2; Length 557;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 NPMNRLVAE 13

Db 296 NPMNRLVAE 304

```
RESULT 17
US-09-949-002-428
; Sequence 428, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 428
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-428

Query Match          50.0%; Score 37; DB 2; Length 578;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 NPMNRLVAE 13
DB      325 NPMNRLTAE 333

RESULT 18
US-08-459-953A-10
; Sequence 10, Application US/08459953A
; Patent No. 6030822
; GENERAL INFORMATION:
; APPLICANT: Lechner, Cornelia
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
; TITLE OF INVENTION: KINASE, SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,953A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,494
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-393-212-10

Query Match          50.0%; Score 37; DB 2; Length 586;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 586 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-953A-10

Query Match          50.0%; Score 37; DB 2; Length 586;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 NPMNRLVAE 13
DB      325 NPMNRLTAE 333

RESULT 19
US-09-393-212-10
; Sequence 10, Application US/09393212
; Patent No. 6579972
; GENERAL INFORMATION:
; APPLICANT: Lechner, Cornelia
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: EXTRACELLULAR SIGNAL-RELATED
; TITLE OF INVENTION: KINASE, SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF PRODUCTION
; AND USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,212
; FILING DATE: 09-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/459,953A
; FILING DATE: June 2, 1995
; APPLICATION NUMBER: 08/029,494
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 586 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-393-212-10

Query Match          50.0%; Score 37; DB 2; Length 586;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
```

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 NPMNRLVAE 13
|||:||||
Db 325 NPMNRLTAE 333

RESULT 20

US-08-905-223-307
; Sequence 307, Application US/08905223
; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric

; APPLICANT: Lacroix, Bruno

; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Win95

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/905,223

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelsen, Ned A.

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 307:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 95 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; ORIGINAL SOURCE:

; ORGANISM: Homo Sapiens

; TISSUE TYPE: Brain

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: -92--1

; IDENTIFICATION METHOD: Von Heijne matrix

; OTHER INFORMATION: score 6.8

; OTHER INFORMATION: seq ILIASSLPTLSHP/AP

US-08-905-223-307

Query Match 48.6%; Score 36; DB 2; Length 95;

Best Local Similarity 80.0%; Pred. No. 34;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 NPMNRLVAET 14

|||||

Db 53 NPMNRLVACT 62

RESULT 21

US-08-583-110-4918

; Sequence 4918, Application US/09583110

; Patent No. 6699703

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

; FILE REFERENCE: PATH00-07A

; CURRENT APPLICATION NUMBER: US/09/583,110

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 4918

; LENGTH: 123

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-09-583-110-4918

Query Match 48.6%; Score 36; DB 2; Length 123;

Best Local Similarity 53.3%; Pred. No. 47;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15

|||||

Db 41 FGVEASMGRIYPETL 55

RESULT 22

US-09-328-352-4939

; Sequence 4939, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 4939

; LENGTH: 196

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-4939

Query Match 48.6%; Score 36; DB 2; Length 196;

Best Local Similarity 42.9%; Pred. No. 81;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAET 14

|||||

Db 21 YALEPMNNAVATDT 34

RESULT 23

US-09-711-164-309

; Sequence 309, Application US/09711164

; Patent No. 6589738

; GENERAL INFORMATION:

; APPLICANT: Forsyth, R. Allyn

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF

; FILE REFERENCE: ELITRA-008A

; CURRENT APPLICATION NUMBER: US/09/711,164

; CURRENT FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/164415

; PRIOR FILING DATE: 1999-11-9

; NUMBER OF SEQ ID NOS: 469

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 309

; LENGTH: 201

; TYPE: PRT

; ORGANISM: Escherichia coli

US-09-711-164-309

Query Match 48.6%; Score 36; DB 2; Length 201;
Best Local Similarity 46.7%; Pred. No. 84;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
|:|:| |:|:| |:|:|
Db 124 FSVEAPKTKLLAQKL 138

RESULT 24

US-09-492-709A-391

; Sequence 391, Application US/09492709A

; Patent No. 6720139

; GENERAL INFORMATION:

; APPLICANT: Zyskind, Judith

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Trawick, John

; APPLICANT: Forsyth, R. Allyn

; APPLICANT: Froelich, Jamie M.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

; TITLE OF INVENTION: ESCHERICHIA COLI

; FILE REFERENCE: ELITRA.001A

; CURRENT APPLICATION NUMBER: US/09/492,709A

; CURRENT FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 485

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 391

; LENGTH: 201

; TYPE: PRT

; ORGANISM: E. Coli

US-09-492-709A-391

Query Match 48.6%; Score 36; DB 2; Length 201;
Best Local Similarity 46.7%; Pred. No. 84;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
|:|:| |:|:| |:|:|
Db 124 FSVEAPKTKLLAQKL 138

RESULT 25

US-09-489-039A-10971

; Sequence 10971, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 10971

; LENGTH: 207

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10971

Query Match 48.6%; Score 36; DB 2; Length 207;
Best Local Similarity 46.7%; Pred. No. 87;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
|:|:| |:|:| |:|:|
Db 130 FSVEAPKTKLLAQKL 144

RESULT 26

US-09-543-681A-7203

; Sequence 7203, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 7203

; LENGTH: 215

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-7203

Query Match 48.6%; Score 36; DB 2; Length 215;
Best Local Similarity 46.7%; Pred. No. 91;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
|:|:| |:|:| |:|:|
Db 138 FSVEAPKTKLLAQKL 152

RESULT 27

US-09-489-039A-13401

; Sequence 13401, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 13401

; LENGTH: 441

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-13401

Query Match 48.6%; Score 36; DB 2; Length 441;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VENPMNRLVAET 14
|:|:| |:|:| |:|:|
Db 160 VENPOHRAAAT 171

RESULT 28

US-09-489-039A-10520

; Sequence 10520, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10520
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10520

Query Match 48.6%; Score 36; DB 2; Length 816;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETL 15
||| ||| ||| |||
Db 360 AVEQMNELLSEYL 373

RESULT 29

US-08-822-445-2
; Sequence 2, Application US/08822445
; Patent No. 5952223
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Jerry
; APPLICANT: Perou, Charles
; APPLICANT: Moore, Karen
; TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,445
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-062-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2186 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-445-2

Query Match 48.6%; Score 36; DB 1; Length 2186;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETL 15
||| ||| ||| |||
Db 1775 AVEQVQRRALETM 1788

RESULT 30

US-09-396-540-2
; Sequence 2, Application US/09396540
; Patent No. 6310182

; GENERAL INFORMATION:
; APPLICANT: Kaplan, Jerry
; APPLICANT: Perou, Charles
; APPLICANT: Moore, Karen
; TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/822,445
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-062-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2186 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-396-540-2

Query Match 48.6%; Score 36; DB 2; Length 2186;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETL 15
||| ||| ||| |||
Db 1775 AVEQVQRRALETM 1788

Search completed: December 17, 2005, 07:34:27
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 07:07:52 ; Search time 186 Seconds
(without alignments)
35.434 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74

Sequence: 1 FAVENPMRLVAETL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	84	4	AAB72616 Canine in
2	74	100.0	115	3	AAY58220 Canine ma
3	74	100.0	134	3	AAY58219 Canine in
4	74	100.0	134	4	AAB72615 Canine in
5	55	74.3	132	2	AAW08479 Ovine IL-
6	46	62.2	427	4	ABG959883 S. cinna
7	43	58.1	159	3	ABG959808 Pepper mi
8	41	55.4	307	4	ABB71894 Drosophil
9	41	55.4	307	8	AD008016 Fly polyyp
10	41	55.4	514	8	ADS27735 Bacterial
11	40	54.1	59	8	ADU47425 Yarrowia
12	39	52.7	518	8	ABG69884 Drosophil
13	39	52.7	559	7	ADF06956 Bacterial
14	39	52.7	756	8	ADJ49966 Oil-assoc
15	39	52.7	804	4	AU34800 E. coli c
16	39	52.7	804	6	ABU28825 Protein e
17	38.5	52.0	711	8	ADN25977 Bacterial
18	38	51.4	59	5	ABP06885 Human ORF
19	38	51.4	252	6	ABU18938 Protein e
20	38	51.4	341	9	ABM94674 M. xanthu
21	38	51.4	549	7	ADH86490 Enterococ
22	38	51.4	664	4	AAE20000 Arabidops
23	38	51.4	860	7	ABO77366 Pseudomon
24	38	51.4	956	4	ABB53002 Escherich

25	38	51.4	1205	7	ABO80130 Pseudomon
26	37.5	50.7	324	9	AEA62655 Mitochond
27	37	50.0	88	5	ABP02493 Human ORF
28	37	50.0	115	2	AAW05273 N-termina
29	37	50.0	115	2	AAW72948 Truncated
30	37	50.0	133	1	AAW71064 Murine eo
31	37	50.0	133	1	AAW72947 B cell di
32	37	50.0	133	1	AAW72947 B cell di
33	37	50.0	133	2	AAW72949 T cell re
34	37	50.0	133	2	AAW72949 T cell re
35	37	50.0	133	2	AAW72947 T cell re
36	37	50.0	133	4	AAW72947 T cell re
37	37	50.0	134	5	ABG94349 Mouse C-I
38	37	50.0	134	5	ABG80661 Mouse IL-
39	37	50.0	134	7	ADK17220 Mouse C-I
40	37	50.0	162	8	ADN47619 Thymococ
41	37	50.0	236	2	AAW24191 Bovine RS
42	37	50.0	246	9	ADW17740 Pinus rad
43	37	50.0	311	6	ABU28549 Protein e
44	37	50.0	311	6	ABU45268 Protein e
45	37	50.0	360	7	ADC61397 Nicotiana
46	37	50.0	448	4	AAW25874 Human pro
47	37	50.0	557	7	ADF45053 Human kin
48	37	50.0	557	8	ADS92972 Mitogen-a
49	37	50.0	558	8	ADS10754 Human the
50	37	50.0	583	9	ADV97853 Murine pr
51	37	50.0	586	7	ADC64460 Human ext
52	37	50.0	586	8	ADG98196 Human ext
53	37	50.0	586	8	ABM84222 Human dia
54	37	50.0	587	6	AAE32021 Human kin
55	37	50.0	587	8	ADS12008 Human the
56	37	50.0	606	4	ABG29655 Novel hum
57	37	50.0	606	4	ABB69121 Drosophil
58	37	50.0	615	8	ADS27325 Bacterial
59	37	50.0	663	8	ADS26595 Bacterial
60	37	50.0	663	8	ADS26970 Bacterial
61	37	50.0	985	4	AAW90623 C glutam
62	37	50.0	1021	3	AAW77728 Human G p
63	37	50.0	1021	3	ADE55164 Human Pro
64	37	50.0	1021	7	ADE55168 Human Pro
65	37	50.0	1021	7	ADE55172 Human Pro
66	37	50.0	1021	7	ADE55176 Human Pro
67	37	50.0	1027	7	ABM85538 Mouse pro
68	37	50.0	1155	4	AAW92010 C glutam
69	37	50.0	1155	7	ADJ87397 DNA repli
70	37	50.0	1155	9	ABE13129 C. glutam
71	37	50.0	1351	4	ABE61727 Drosophil
72	37	50.0	1459	7	ADC26275 Human NOV
73	37	50.0	1478	5	AAU10540 Rat CIRL-
74	37	50.0	1478	7	ADD46680 Rat Prote
75	37	50.0	1488	7	ADE55162 Rat Prote
76	37	50.0	1488	7	ADE55174 Rat Prote
77	37	50.0	1488	7	ADE55170 Rat Prote
78	37	50.0	1488	7	ADE55166 Rat Prote
79	37	50.0	1488	8	ADM97582 Human cal
80	37	50.0	1878	4	ABB61852 Drosophil
81	37	50.0	2092	6	ABJ25403 Aspergill
82	37	50.0	2092	6	ABJ26003 Aspergill
83	36.5	49.3	288	8	ADT59574 Plant pol
84	36	48.6	77	4	ABB41650 Peptide #
85	36	48.6	77	4	AAW35444 Peptide #
86	36	48.6	77	4	AAW75331 Human bon
87	36	48.6	77	4	AAW62520 Human bra
88	36	48.6	77	4	ABG57088 Human liv
89	36	48.6	95	2	AAW13023 Human sec
90	36	48.6	123	8	ADK48403 Streptoco
91	36	48.6	146	4	AAU03698 Group B S
92	36	48.6	155	4	ABG07176 Novel hum
93	36	48.6	175	3	AAW53339 Human col
94	36	48.6	196	4	ADA33652 Acinetoba
95	36	48.6	197	4	AAW73901 Human col
96	36	48.6	200	6	ABU45632 Protein e
97	36	48.6	201	3	AAW16033 E. coli p

98 36 48.6 201 4 AAU34765
99 36 48.6 201 4 AAU38380
100 36 48.6 201 4 AAG98839
101 36 48.6 201 4 AAG98839
102 36 48.6 201 6 ABU50212
103 36 48.6 201 6 ABU40982
104 36 48.6 201 6 ABU31401
105 36 48.6 201 6 ABU47784
106 36 48.6 201 6 ABU27723
107 36 48.6 201 7 ABU14733
108 36 48.6 201 7 ABU64454
109 36 48.6 215 8 ADF06918
110 36 48.6 220 8 ADY06460
111 36 48.6 221 8 ADN74015
112 36 48.6 254 4 ABU06072
113 36 48.6 255 4 AAE04891
114 36 48.6 255 5 ABP51810
115 36 48.6 257 6 ABP78820
116 36 48.6 258 3 AAB41622
117 36 48.6 266 8 ADN19554
118 36 48.6 309 4 ABG17090
119 36 48.6 346 8 ADY08364
120 36 48.6 363 4 ADG27800
121 36 48.6 375 6 AB07634
122 36 48.6 418 6 ABU31504
123 36 48.6 441 7 AB066884
124 36 48.6 477 6 ABU23254
125 36 48.6 486 5 ABB47843
126 36 48.6 513 7 ABP25425
127 36 48.6 571 8 ADV88216
128 36 48.6 571 8 ADV79469
129 36 48.6 571 8 ADV81641
130 36 48.6 571 8 ADV81641
131 36 48.6 603 6 ABU45042
132 36 48.6 641 6 ABJ25373
133 36 48.6 654 5 ABB92841
134 36 48.6 717 6 ABJ25973
135 36 48.6 730 9 AEA49153
136 36 48.6 803 4 ABU28371
137 36 48.6 804 4 AAU38327
138 36 48.6 804 6 ABU48260
139 36 48.6 816 7 AB064003
140 36 48.6 1079 4 ABB71337
141 36 48.6 1175 8 ADS44237
142 36 48.6 1447 8 ADN2331
143 36 48.6 2186 2 AAU31948
144 36 48.6 3672 2 AAU31950
145 36 48.6 3788 2 AAU23594
146 36 48.6 3801 2 AAU31949
147 36 48.6 3801 8 ADRI4706
148 35 47.3 37 7 ADD35447
149 35 47.3 59 8 ADU47422
150 35 47.3 75 8 ADR94734

ALIGNMENTS

RESULT 1
AAB72616
ID AAB72616 standard; protein; 84 AA.

XX
AC AAB72616;

XX
DT 04-MAY-2001 (first entry)

XX
DE Canine interleukin-5 protein #2.

XX
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
XX inflammatory reaction.

XX
OS Canis sp.

Aau34765 E. coli c
Aau38380 Salmonell
Aag98839 E. coli g
Aag98839 Escherich
Abu50212 Protein e
Abu40982 Protein e
Abu31401 Protein e
Abu47784 Protein e
Abu27723 Protein e
Abu14733 Protein e
Abu64454 Klebsiell
Adf06918 Bacterial
Ady06460 Plant ful
Adn74015 Thale cre
Auo06072 N. mening
Aao04891 Human tra
Abp51810 Human pot
Abp78820 N. gonorr
Aab41622 Human ORF
Adn19554 Bacterial
Abg17090 Novel hum
Ady08364 Plant ful
Adg27800 Human nov
Ab07634 Allolococ
Abu31504 Protein e
Ab066884 Klebsiell
Abb47843 Listeria
Ado55911 Bacillus
Abp25425 Streptoco
Adv88216 Streptoco
Adv79469 Streptoco
Adv81641 Streptoco
Abj25373 Aspergill
Abb92841 Herbicida
Abj25973 Aspergill
Aea49153 L. rhamo
Aau28371 Protein e
Aau38327 Salmonell
Abu48260 Protein e
Ab064003 Klebsiell
Abb71337 Drosophil
Ads44237 Bacterial
Adn2331 Bacterial
Aaw31948 Mouse 22B
Aaw31950 Human bg
Aaw23594 Murine ly
Aaw31949 Human bg
Adri4706 Human NF-
Add35447 Streptoco
Adu47422 Saccharom
Adr94734 Novel S.

PN WO200111049-A2.
XX 15-FEB-2001.
XX 09-AUG-2000; 2000WO-US021651.
XX 10-AUG-1999; 99US-00371615.
XX (IDEX-) IDEXX LAB INC.
PA Guo H, Lawton R, Mermer B, Aiyappa AP;
PI WPI; 2001-191542/19.
DR N-PSDB; AAF74305.
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
XX generating antibodies which are useful in treating allergies in dogs.
XX Example 1; Fig 1; 48pp; English.
XX The present invention provides the protein and coding sequences of the
XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
XX cancer and inflammatory reactions in dogs. The present sequence is one
XX version of the IL-5 protein shown in the specification
XX Sequence 84 AA;
SQ
Query Match 100.0%; Score 74; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMRLVAETL 15
DB 20 FAVENPMRLVAETL 34
|||||
RESULT 2
AAY58220
ID AAY58220 standard; protein; 115 AA.
XX
AC AAY58220;
XX 14-MAR-2000 (first entry)
XX
XX Canine mature interleukin-5 (IL-5).
DE Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
PN
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR N-PSDB; AA255550, AA255551.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX Claim 3h; Page 227; 264pp; English.
XX
XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
XX -5 (IL-5). The invention relates to canine IL-4, canine or feline Fit-3
CC

CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides
 CC which encode these immunoregulatory proteins. The proteins, their
 CC associated nucleic acids, specific antibodies and inhibitors may be used
 CC as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 115 AA;

Query Match 100.0%; Score 74; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 8.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15

Db 1 FAVENPMNRLVAETL 15

RESULT 3

AA58219
 ID AAY58219 standard; protein; 134 AA.

XX AC AAY58219;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5).

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX OS Canis familiaris.

XX FN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 98WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX DR N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 3h; Page 224; 264pp; English.

XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
 CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Fit-3
 CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides
 CC which encode these immunoregulatory proteins. The proteins, their
 CC associated nucleic acids, specific antibodies and inhibitors may be used
 CC as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 134 AA;

Query Match 100.0%; Score 74; DB 3; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15

Db 20 FAVENPMNRLVAETL 34

RESULT 4

AA872615
 ID AAB72615 standard; protein; 134 AA.

XX AC AAB72615;

XX DT 04-MAY-2001 (first entry)

XX DE Canine interleukin-5 protein #1.

XX KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 KW inflammatory reaction.

XX OS Canis sp.

XX FN WO200111049-A2.

XX PD 15-FEB-2001.

XX PF 09-AUG-2000; 2000WO-US021651.

XX PR 10-AUG-1999; 99US-00371615.

XX PA (IDEX-) IDEX LAB INC.

XX PI Guo H, Lawton R, Mermer B, Aiyappa AP;

XX WPI; 2001-191542/19.

XX DR N-PSDB; AAF74300.

XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
 PT generating antibodies which are useful in treating allergies in dogs.

XX PS Claim 29; Page 46-47; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 protein shown in the specification

XX Sequence 134 AA;

Query Match 100.0%; Score 74; DB 4; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15

Db 20 FAVENPMNRLVAETL 34

RESULT 5

AAW08479

Db 161 FSVBPMGSLVAE 173

RESULT 7
ABB08908
ID ABB08908 standard; protein; 159 AA.
XX AC ABB08908;
XX DT 28-JUN-2002 (first entry)
XX DE Pepper mild mottle virus envelope protein.
XX KW Pepper mild mottle virus; PMMV; envelope; Tobamovirus; transgenic plant;
XX KW plant expression vector; transgenic.
XX OS Pepper mild mottle virus.
XX PN KR149216-B1.
XX PD 17-AUG-1998.
XX PF 11-NOV-1994; 94KR-00029486.
XX PR 11-NOV-1994; 94KR-00029486.
XX PA (POHA-) POHANG ENG COLLEGE.
XX PI Nam H, Choe J, Lee H, Park Y, Kim C;
XX DR WPI; 2000-252824/22.
XX DR N-PSDB; ABA97721.
XX PT ENVELOPE GENE OF PEPPER MILD MOTTLE VIRUS.
XX PS Claim 2; Page 8; 12pp; Korean.
XX CC The invention relates to the envelope gene (ABA97721) and protein (ABB08908) from pepper mild mottle virus (PMMV - a member of the Tobamovirus family of single-stranded RNA viruses). The invention also encompasses plant expression vectors which comprise the PMMV envelope gene. The present sequence represents the PMMV envelope protein

SQ Sequence 159 AA;
Query Match 58.1%; Score 43; DB 3; Length 159;
Best Local Similarity 69.2%; Pred. No. 9.9;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
||| |
Dp 97 VENPQNPTTAETL 109

RESULT 8
ABB71894
ID ABB71894 standard; protein; 307 AA.
XX AC ABB71894;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 42474.
XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX

PF 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL15997.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
XX PS Disclosure; SEQ ID NO 42474; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 307 AA;
Query Match 55.4%; Score 41; DB 4; Length 307;
Best Local Similarity 64.3%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
||| |
Dp 59 AVRNPRRLTVEVL 72

RESULT 9
ADO08016
ID ADO08016 standard; protein; 307 AA.
XX AC ADO08016;
XX DT 01-JUL-2004 (first entry)
XX DE Fly polypeptide #58.
XX KW Fly; fat cell number; fat cell size; obesity; diabetes; anorectic; antidiabetic.
XX OS Diptera.
XX PN US2004071700-A1.
XX PD 15-APR-2004.
XX PF 09-OCT-2002; 2002US-00267502.
XX PR 09-OCT-2002; 2002US-00267502.
XX PA (LIFE-) LIFE SCI DEV CORP.
XX PI Kim J, Galant R;
XX DR WPI; 2004-328526/30.
XX DR N-PSDB; ADO07799.
XX PT Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the

XX New isolated orotate-phosphoribosyl transferase polynucleotides and
PT polypeptides, useful for producing and selecting yeast strains capable of
PT stable genetic integration of heterologous sequences into a host genome.
XX
PS Example 1; SEQ ID NO 20; 38pp; English.
XX
CC The present invention provides polypeptides encoding a novel orotate-
CC phosphoribosyl transferase (URA5) gene. The invention is useful for
CC producing and selecting yeast strains capable of stable genetic
CC integration of heterologous sequences into a host genome. The invention
CC is also useful for measuring expression of the SC87 gene and secretory
CC pathway (SEC65) gene and to further characterise the structure and
CC function of this gene and its encoded protein. The nucleic acid fragments
CC of the invention can also be used as probes for various hybridisation
CC techniques. The present sequence is Yarrowia lipolytica SEC65-related
CC protein.
XX
XX Sequence 59 AA;

Query Match 54.1%; Score 40; DB 8; Length 59;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AVENPMRLVAE 13
Db |||||: :|||
22 AVENPLGQTIAE 33

RESULT 12
ABB69884
ID ABB69884 standard; protein; 518 AA.
XX
AC ABB69884;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 36444.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL13987.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 36444; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 518 AA;

Query Match 52.7%; Score 39; DB 4; Length 518;
Best Local Similarity 60.0%; Pred. No. 2.Se+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETL 15
Db |||||: :|||
47 FRVERDQYKLVAE 61

RESULT 13
ADF06956
ID ADF06956 standard; protein; 559 AA.
XX
AC ADF06956;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polypeptide #3069.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
OS Proteus mirabilis.
XX
PN US6605709-B1.
XX
PD 12-AUG-2003.
XX
PF 05-APR-2000; 2000US-00543681.
XX
PR 09-APR-1999; 99US-0128706P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL;
XX
DR WPI; 2003-895291/82.
DR N-PSDB; ADF02784.
XX
PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
PS Disclosure; SEQ ID NO 7241; 870pp; English.
XX
CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
XX Sequence 559 AA;

Query Match 52.7%; Score 39; DB 7; Length 559;
Best Local Similarity 42.9%; Pred. No. 2.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAET 14
Db |||||: :|||: :|||

```

Db          397 PSLEKPVNRLINT 410
RESULT 14
ADJ49966
ID ADJ49966 standard; protein; 756 AA.
XX
AC ADJ49966;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #1466.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
PN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
(LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
XX
PS Example 3; SEQ ID NO 1970; 22pp; English.
XX
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 756 AA;
XX
Query Match 52.7%; Score 39; DB 8; Length 756;
Best Local Similarity 63.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 FAVENPMNRLV 11
Db ||||| :
67 FAKENPMNVL 77
RESULT 15
AAU34800
ID AAU34800 standard; protein; 804 AA.
XX
AC AAU34800;
XX
DT 14-FEB-2002 (first entry)
XX
DE E. coli cellular proliferation protein #381.

```

```

XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
OS Escherichia coli.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX
PR 23-MAY-2000; 2000US-0206848P.
XX
PR 26-MAY-2000; 2000US-020727P.
XX
PR 23-OCT-2000; 2000US-0242578P.
XX
PR 27-NOV-2000; 2000US-0253625P.
XX
PR 22-DEC-2000; 2000US-0257931P.
XX
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
DR N-PSDB; AAS52659.
XX
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
PS Example 3; SEQ ID NO 10393; 511pp; English.
XX
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 804 AA;
XX
Query Match 52.7%; Score 39; DB 4; Length 804;
Best Local Similarity 64.3%; Pred. No. 4.2e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 AVENPMNRLVAETL 15
Db ||||| :
348 AVEQQMNELLAEVL 361
RESULT 16
ABU28825
ID ABU28825 standard; protein; 804 AA.
XX
AC ABU28825;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #14352.
XX

```


Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 2 AVENPMNR-LVAETL 15
| :||:| | :||:| |
Db 605 AEDNPLNRLIAEQL 619

RESULT 18
ABP06885
ID ABP06885 standard; protein; 59 AA.
XX ABP06885;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:13752.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myaesthesia gravis.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach WD;
XX
PI WPI; 2002-106308/14.
DR N-PSDB; ABN22637.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 13752; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative diseases, diabetes mellitus, systemic
CC transplantation, cardiovascular diseases, hypothyroidism, cholesterol ester
CC lupus erythematosus, hypertension, immune deficiencies and disorders, infectious
CC storage disease, various immune deficiencies and disorders, rheumatoid
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myaesthesia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 59 AA;
Query Match 51.4%; Score 38; DB 5; Length 59;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 3 VENPMNRLVAET 14
: ||:| | :||:| |
Db 42 IRNPVSRLIAT 53

RESULT 19
ABU18938
ID ABU18938 standard; protein; 252 AA.
XX ABU18938;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #4465.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Bacillus anthracis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA22808.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 46862; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

Query Match 51.4%; Score 38; DB 9; Length 341;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;

DT 28-MAR-2001 (first entry)
 XX Arabidopsis acyl-CoA oxidase ATACX1.
 XX Acyl-CoA oxidase; ACOX; ATACX1; fatty acid; beta-oxidation;
 KW transgenic plant; lipid; vegetable oil.
 XX Arabidopsis thaliana.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 519 /note= "encoded by CCT"
 FT
 XX
 XX WO200075350-A2.
 XX
 PD 14-DEC-2000.
 XX
 XX 08-JUN-2000; 2000WO-US016149.
 PF
 XX
 XX 08-JUN-1999; 99US-0138162P.
 PR
 XX (CALJ) CALGENE LLC.
 PA
 XX Dehesh K;
 XX
 XX WPI; 2001-091217/10.
 DR N-PSDB; AAA89274.
 XX
 XX Polynucleotide encoding proteins involved in fatty acid beta-oxidation,
 PT useful for modifying oil or lipid composition in host plant cells.
 FT
 XX
 XX Claim 27; Page 33-35; 59pp; English.
 XX
 CC The present sequence is that of ATACX1, an acyl-CoA oxidase (ACOX) of
 CC Arabidopsis thaliana. ACOX enzymes catalyzes the initial step of fatty
 CC acid beta-oxidation. The invention provides ACOX and 3-ketoacyl-CoA
 CC thiolase (thiolase) isolated DNA sequences (see AAA89273-85) and encoded
 CC polypeptides (see AAB19999-B20011), and methods of producing such
 CC polypeptides using recombinant methods in host (bacterial, insect,
 CC mammalian and especially plant) cells. Expression of ACOX and/or thiolase
 CC in a plant can be increased or suppressed using nucleic acid constructs
 CC in sense or antisense orientation. This provides a means of manipulating
 CC the content and composition of fatty acids and compounds containing such
 CC fatty acids, such as oils, waxes, fats and storage proteins. Suppression
 CC of ACOX and/or thiolase expression also provides a means of inhibiting or
 CC postponing seed germination
 XX
 XX Sequence 664 AA;
 SQ
 Query Match 51.4%; Score 38; DB 4; Length 664;
 Best Local Similarity 60.0%; Pred. NO. 5.2e+02;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 FAVENPMNRLVAETL 15
 Db 32 FDVSNRMSRLVANDL 46
 RESULT 23
 ABO77366
 ID ABO77366 standard; protein; 860 AA.
 XX
 AC ABO77366;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX Pseudomonas aeruginosa polypeptide #9541.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 KW
 XX Pseudomonas aeruginosa.
 OS
 XX US6551795-B1.
 PN

XX 22-APR-2003.
 PD
 XX 18-FEB-1999; 99US-00252991.
 PF
 XX 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI WPI; 2003-615309/58.
 FT N-PSDB; ABD10937.
 DR
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 FT
 XX Disclosure; SEQ ID NO 26112; 455pp; English.
 PS
 XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84336 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 XX Sequence 860 AA;
 SQ
 Query Match 51.4%; Score 38; DB 7; Length 860;
 Best Local Similarity 58.3%; Pred. NO. 7.2e+02;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 4 ENPMNRLVAETL 15
 Db 744 DNPVNQLVAKGL 755
 RESULT 24
 ABB53002
 ID ABB53002 standard; protein; 956 AA.
 XX
 AC ABB53002;
 XX
 XX 11-FEB-2002 (first entry)
 DT
 XX Escherichia coli polypeptide SEQ ID NO 1353.
 DE
 XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
 KW systemic infection; non-diarrhoeal infection; septicemia;
 KW pyelonephritis; antibiotic resistance.
 XX
 XX Escherichia coli.
 OS
 XX WO200166572-A2.
 PN
 XX 13-SEP-2001.
 PD
 XX 12-MAR-2001; 2001WO-BF003445.
 PF
 XX 10-MAR-2000; 2000PR-00003145.
 PR

CC polynucleotide-packaging polypeptide comprising high mobility group (HMG)
 CC box domains and a protein transduction domain operably linked to a
 CC targeting signal for directing the recombinant polynucleotide-packaging
 CC polypeptide to an intracellular organelle, where the polypeptide
 CC associates with about 10-100 nucleotides of the polynucleotide and
 CC packages the polynucleotide for delivery to the targeted organelle. The
 CC invention also relates to a recombinant high mobility protein or its
 CC fragment comprising a protein transduction domain operably linked to a
 CC targeting signal for a non-nuclear organelle, where the recombinant high
 CC mobility protein associates with a polynucleotide under low stringency
 CC conditions and packages the polynucleotide for delivery to the non-
 CC nuclear organelle, a method of packaging a polynucleotide involving
 CC combining a polynucleotide with an amount of a recombinant polypeptide
 CC sufficient to package the polynucleotide, where the recombinant
 CC polypeptide comprises two or more HMG box domains and a protein
 CC transduction domain operably linked to an organelle targeting signal, a
 CC method of delivering a polynucleotide to an organelle of a cell and a
 CC method of treating a host involving contacting at least one of the host's
 CC cells with a complex comprising an amount of a recombinant polypeptide
 CC effective to package a polynucleotide encoding a therapeutic polypeptide.
 CC The compositions are useful for treating gene related diseases or
 CC disorders chosen from cancer, Alzheimers disease, Parkinsons disease,
 CC hypercholesterolemia, cystic fibrosis, anemia, diabetes, arthritis and
 CC autoimmune diseases, and for treating diseases caused by mitochondrial
 CC genetic defects or abnormalities such as Alpers disease, beta-oxidation
 CC defects, carnitine-acyl-carnitine deficiency, mitochondrial cytopathy and
 CC myogastrointestinal encephalomyopathy. This sequence represents a
 CC mitochondrial localization signal used in the scope of the invention.

XX Sequence 324 AA;

Query Match 50.7%; Score 37.5; DB 9; Length 324;

Best Local Similarity 45.0%; Pred. No. 2.7e+02;

Matches 9; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 1 FAVENP-----MRLVAE 13

Db 290 FTAENPLHQPSPSLNKLVAE 309

RESULT 27

ABP02493

ID ABP02493 standard; protein; 88 AA.

XX AC ABP02493;

XX 25-JUN-2002 (first entry)

XX DE Human ORFX protein sequence SEQ ID NO:4968.

XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

OS Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

XX 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX PI

XX

DR WPI; 2002-106308/14.

DR N-PSDB; ABN18245.

XX

PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.

XX

PS Disclosure; SEQ ID NO 4968; 1037pp; English.

XX

CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 88 AA;

Query Match 50.0%; Score 37; DB 5; Length 88;

Best Local Similarity 50.0%; Pred. No. 66;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETL 15

Db 12 DNPVNRVTVEAM 23

RESULT 28

AAW05273

ID AAW05273 standard; protein; 115 AA.

XX AC AAW05273;

XX 25-MAR-2003 (revised)

DT 12-NOV-1996 (first entry)

XX

DE N-terminally truncated T cell replacing factor (19-133).

XX

KW BCGF II; B cell growth factor; T cell replacing factor; TCR;
 KW B cell differentiation factor; N-terminal truncation; mutant; variant;
 KW modification; cancer; autoimmune disease; infection; treatment;
 KW diagnosis; prevention.

XX

OS Mammalia.

XX

XX Key Location/Qualifiers

FT Protein 1..115

FT /note= "corresponds to TCR protein from which the first

FT 18 N-terminal amino acids have been deleted"

XX

FN JF08067698-A.

XX

XX 12-MAR-1996.

XX

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PF 04-JUL-1986; 95JP-00195345.
XX
XX 04-JUL-1986; 86JP-00157227.
XX
XX (MOTO/) MOTOCHIKA T.
XX
XX WPI; 1996-196574/20.
XX
XX N-PSDB; AAT14922.
XX
XX B cell differentiation factor designated T cell replacing factor (TRF) -
XX useful for prevention, diagnosis and treatment of infectious and
XX auto-immune diseases and cancer.
XX
XX Claim 4; Page 2-3; 1ipp; Japanese.
XX
XX The present sequence is that of an N-terminally truncated form of a
XX protein designated T cell replacing factor (TCR) which has B cell growth
XX factor (BCGF II) activity. The truncated protein, deleted up to and
XX including amino acid residue Ala18, can be used, in common with the full-
XX length protein for prevention, diagnosis and treatment of infectious
XX diseases, autoimmune diseases and certain cancers. (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX
XX Sequence 115 AA;
SQ
Query Match 50.0%; Score 37; DB 2; Length 115;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
DB 2 AMEIPMSTVVKETL 15
|:| |:| |:| |:|
|:| |:| |:| |:|

RESULT 29
AAW72948
ID AAW72948 standard; protein; 115 AA.
XX
XX AAW72948;
XX
XX 21-JAN-1999 (first entry)
XX
XX Truncated T cell replacing factor.
XX
XX Mouse; T cell replacing factor; TRF; B cell growth factor; BCGF;
XX B cell differentiation activating factor; B cell differentiating factor.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1 /label= optional
XX
XX Misc-difference 2 /label= optional
XX
XX Misc-difference 3 /label= optional
XX
XX JP10262673-A.
XX
XX 06-OCT-1998.
XX
XX 04-JUL-1986; 97JP-00055274.
XX
XX 04-JUL-1986; 95JP-00195345.
XX
XX (HONJ/) HONJO T.
XX
XX WPI; 1998-587290/50.
XX
XX Preparation of B cell differentiating factor - by culturing transformed
XX cells containing plasmids with DNA encoding the factor.
XX
XX Claim 6; Page 3; 10pp; Japanese.

XX The present sequence represents a truncated T cell replacing factor (full
XX length given in AAW72947) having B cell growth factor activity. A method
XX has been developed for the preparation of B cell differentiation
XX activating factor (also designated BCGF. B cell growth factor, T cell
XX replacing factor and TRF). The method comprises producing a protein by
XX culturing a transformed cell introduced by a plasmid containing a DNA
XX coding B cell differentiation activating factor. The method is used for
XX the large scale preparation of B cell differentiating factor
XX
XX Sequence 115 AA;
SQ
Query Match 50.0%; Score 37; DB 2; Length 115;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
DB 2 AMEIPMSTVVKETL 15
|:| |:| |:| |:|
|:| |:| |:| |:|

RESULT 30
AAP71064
ID AAP71064 standard; protein; 133 AA.
XX
XX AAP71064;
XX
XX 25-MAR-2003 (revised)
XX
XX 13-MAY-1991 (first entry)
XX
XX Murine eosinophil differentiation factor (EDF).
XX
XX EDA; B-cell growth factor II; BCGF II; haemopoiesis; myeloma cells;
XX eosinophilia; interleukin.
XX
XX Mus musculus.
XX
XX W08704466-A.
XX
XX 30-JUL-1987.
XX
XX 15-JAN-1987; 87WO-GB0000021.
XX
XX 15-JAN-1986; 86GB-00000835.
XX
XX 15-JAN-1986; 86GB-00000836.
XX
XX (AMSH ) AMERSHAM INT PLC.
XX
XX Sanderson CJ, Young IG;
XX
XX WPI; 1987-221267/31.
XX
XX Eosinophil differentiation factor - with eosinophil differentiation
XX activity and B cell growth promoting activity of B cell growth factor II.
XX
XX Claim 7; Fig 5; 37pp; English.
XX
XX The EDF gene product is a novel interleukin, useful in the study of
XX haemopoiesis and B-cell differentiation, and may have utility in MAb
XX production. It may be used therapeutically in regulation of the immune
XX response, and promotion of eosinophilia. See also AAN71243. (Updated on
XX 25-MAR-2003 to correct PA field.)
XX
XX Sequence 133 AA;
SQ
Query Match 50.0%; Score 37; DB 1; Length 133;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
DB 20 AMEIPMSTVVKETL 33
|:| |:| |:| |:|
|:| |:| |:| |:|

```

Search completed: December 17, 2005, 07:29:05
Job time : 194 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 07:21:37 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74

Sequence: 1 PAVENPMRLVAETL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	74.3	134	2 JCS116	interleukin-5 prec
2	43	58.1	157	1 VCTMPV	coat protein - pep
3	41	55.4	514	2 A87266	sensor histidine k
4	40	54.1	310	2 JCS516	signal recognition
5	40	54.1	447	1 E69878	RNA-binding Sun pr
6	40	54.1	1944	2 AH3098	rhizobiotin/RTX to
7	40	54.1	1990	2 A96188	probable phosphos
8	39	52.7	158	2 A60023	coat protein - odo
9	39	52.7	158	2 S14468	coat protein - odo
10	39	52.7	158	2 JQ1266	coat protein - odo
11	39	52.7	221	2 T02666	germin-like protei
12	39	52.7	756	2 JCS590	cycloartenol synth
13	39	52.7	804	1 ISECTB	DNA topoisomerase
14	39	52.7	804	2 B91208	hypothetical prote
15	39	52.7	804	2 D86054	germin-like protei
16	38	51.4	181	2 T02591	probable rna matur
17	38	51.4	773	2 T40694	probable sensor/re
18	38	51.4	786	2 F83292	hypothetical prote
19	37	50.0	50	2 H97798	hypothetical prote
20	37	50.0	132	1 A48418	interleukin-5 prec
21	37	50.0	133	1 ICMS5	coat protein mutan
22	37	50.0	159	4 S34856	hypothetical prote
23	37	50.0	162	1 D71206	hypothetical prote
24	37	50.0	162	2 H75019	probable tRNA synt
25	37	50.0	311	2 E85565	probable tRNA synt
26	37	50.0	311	2 B90715	purine nucleosidas
27	37	50.0	311	2 A64800	protein kinase ERK
28	37	50.0	493	2 B42519	
29	37	50.0	557	2 S23429	

30	37	50.0	650	2 T41681	probable serine/th
31	37	50.0	943	2 T33795	hypothetical prote
32	37	50.0	1304	2 T14073	dynein lb heavy ch
33	37	50.0	1384	2 T18366	latrophilin-2, apl
34	37	50.0	1397	2 T18377	latrophilin-2 (apl
35	37	50.0	1399	2 T18370	latrophilin-2 (apl
36	37	50.0	1412	2 T18380	latrophilin-2 (apl
37	37	50.0	1450	2 T18382	latrophilin-2 (apl
38	37	50.0	1452	2 T17157	CL2AA protein - ra
39	37	50.0	1463	2 T18386	latrophilin-2 (apl
40	37	50.0	1463	2 T17159	CL2AC protein - ra
41	37	50.0	1465	2 T18384	latrophilin-2 (apl
42	37	50.0	1467	2 T17160	CL2BA protein - ra
43	37	50.0	1478	2 T18388	latrophilin-2 (apl
44	37	50.0	1478	2 T17185	CL2BC protein - ra
45	37	50.0	1487	2 T14324	alpha-latotoxin r
46	37	50.0	2510	2 T28160	hypothetical prote
47	36	48.6	157	2 AH3460	arsenate reductase
48	36	48.6	166	2 T42290	hypothetical prote
49	36	48.6	200	2 G82139	endopeptidase Clp
50	36	48.6	201	1 R5EB4Y	ribosomal protein
51	36	48.6	201	1 R5EC4	ribosomal protein
52	36	48.6	201	2 AB1006	50S ribosomal chai
53	36	48.6	201	2 H91151	ribosomal protein
54	36	48.6	201	2 D85937	ribosomal protein
55	36	48.6	201	2 AC0026	50S ribosomal prot
56	36	48.6	247	2 H69374	NH(3)-dependent NA
57	36	48.6	251	2 H72275	phosphate ABC tran
58	36	48.6	255	2 A81099	1-acyl-sn-glycerol
59	36	48.6	255	2 A81842	1-acylglycerol-3-p
60	36	48.6	255	2 S70545	1-acylglycerol-3-p
61	36	48.6	266	2 S67435	phosphoadenyl-su
62	36	48.6	360	2 AF0247	probable exported
63	36	48.6	387	2 H88941	protein R13D11.4 l
64	36	48.6	394	2 H87640	sensor histidine k
65	36	48.6	486	2 A81575	acetaldehyde dehyd
66	36	48.6	486	2 AC1222	acetaldehyde dehyd
67	36	48.6	513	2 H69735	endo-1,4-beta-xyla
68	36	48.6	596	2 A11865	hypothetical prote
69	36	48.6	615	2 D87344	60 kd inner-membra
70	36	48.6	651	2 C75014	hypothetical prote
71	36	48.6	654	2 F85057	receptor-like prot
72	36	48.6	804	2 AD0958	DNA Gyrase chain B
73	36	48.6	1089	2 T31583	hypothetical prote
74	36	48.6	1140	2 T41457	dna repair protein
75	36	48.6	1447	2 T15200	hypothetical prote
76	36	48.6	3788	2 T30851	lysosomal traffick
77	36	48.6	3788	2 T13960	beige protein homo
78	35	47.3	139	2 E72559	hypothetical prote
79	35	47.3	163	2 E90212	conserved hypotet
80	35	47.3	185	2 C95109	ribosome recycling
81	35	47.3	185	2 F97977	ribosome recycling
82	35	47.3	227	2 S52856	Arac-like protein
83	35	47.3	251	2 A82749	transcription regu
84	35	47.3	254	2 E84528	uracase accessory p
85	35	47.3	256	2 D71979	signal recognition
86	35	47.3	273	2 S21731	probable hydroxybu
87	35	47.3	276	2 C95891	transcription regu
88	35	47.3	278	2 D97530	hypothetical prote
89	35	47.3	286	2 G95301	conserved hypotet
90	35	47.3	288	2 D69480	two-component sens
91	35	47.3	334	2 H84138	cytochrome d ubiq
92	35	47.3	378	2 A82406	ribosomal protein
93	35	47.3	390	2 S54026	branched chain ani
94	35	47.3	405	2 T50717	probable O-antigen
95	35	47.3	410	2 AH0051	gamma-glutamyl pho
96	35	47.3	416	2 AH0543	glutamate-5-semial
97	35	47.3	417	1 RDECEB	gamma-glutamylphos
98	35	47.3	417	2 D85513	gamma-glutamylphos
99	35	47.3	417	2 F90662	probable fibrial
100	35	47.3	441	2 AC0544	conserved domain p
101	35	47.3	442	2 B35145	hypothetical prote
102	35	47.3	447	2 H98012	

103 35 47.3 449 2 JC1137
104 35 47.3 449 2 S18561
105 35 47.3 479 2 G75092
106 35 47.3 484 2 AE3176
107 35 47.3 493 2 C36415
108 35 47.3 493 2 T37405
109 35 47.3 493 2 A36850
110 35 47.3 493 2 T28560
111 35 47.3 493 2 H72165
112 35 47.3 496 2 AD3085
113 35 47.3 496 2 E98201
114 35 47.3 499 2 B75577
115 35 47.3 513 2 A33966
116 35 47.3 532 2 S40983
117 35 47.3 537 2 AF0575
118 35 47.3 544 2 S61302
119 35 47.3 591 2 S73790
120 35 47.3 649 2 T47609
121 35 47.3 664 2 G84771
122 35 47.3 682 2 B86336
123 35 47.3 747 2 F88561
124 35 47.3 759 2 E81869
125 35 47.3 886 2 B83306
126 35 47.3 1040 2 AH1926
127 35 47.3 1377 2 T19214
128 34.5 46.6 256 2 B93383
129 34.5 46.6 327 2 T04004
130 34.5 46.6 427 2 AE2851
131 34.5 46.6 427 2 C97628
132 34 45.9 90 2 H83931
133 34 45.9 111 2 T51568
134 34 45.9 144 2 T51597
135 34 45.9 154 2 AB2509
136 34 45.9 158 1 VCTMKO
137 34 45.9 158 2 S49435
138 34 45.9 158 2 S55374
139 34 45.9 158 2 S55374
140 34 45.9 159 1 VCTMVU
141 34 45.9 159 2 D81158
142 34 45.9 159 2 H81946
143 34 45.9 166 1 B71033
144 34 45.9 166 2 A75181
145 34 45.9 219 1 A39574
146 34 45.9 241 1 JQ1641
147 34 45.9 257 2 S70544
148 34 45.9 264 2 C84971
149 34 45.9 267 2 AG0208
150 34 45.9 271 2 S18730

ALIGNMENTS

RESULT 1
JC5116
interleukin-5 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: JC5116
R/Mertens, B.; Gobright, E.; Seow, H.F.
Gene 176, 273-274, 1996
A>Title: The nucleotide sequence of the bovine interleukin-5 encoding cDNA.
A:Reference number: JC5116; MUID:97075944; PMID:8918267
A:Molecule type: mRNA
A:Residues: 1-134 <MER>
A:Cross-references: UNIPROT:P52173; UNIPARC:UPI000012D4CB; EMBL:Z67872; NID:g1113120; PI
C/Comment: This protein plays a role in the eosinophilia associated with parasitic disea
C:Genetics:
A/Gene: IL-5
C:Superfamily: interleukin-5
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-134/Product: interleukin-5 #status predicted <MAT>
F:63/Disulfide bonds: interchain (to 105) #status predicted
F:76,90/Binding site: carbohydrate (Asn) (Covalent) #status predicted
F:105/Disulfide bonds: interchain (to 63) #status predicted
Query Match 74.3%; Score 55; DB 2; Length 134;
Best Local Similarity 85.7%; Pred. No. 0.015;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 AVENPMNRLVAETL 15
DB 21 AVESTMNLVAETL 34
|||||
RESULT 2
VCTMPV
coat protein - pepper mild mottle virus (strain Spain)
C:Species: pepper mild mottle virus
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: JQ1315
R:Alonso, E.; Garcia-Luque, I.; de la Cruz, A.; Wicke, B.; Avila-Rincon, M.J.; Serra, M.
J. Gen. Virol. 72, 2875-2884, 1991
A>Title: Nucleotide sequence of the genomic RNA of pepper mild mottle virus, a resistant
A:Reference number: JQ1312; MUID:92113528; PMID:1765765
A:Accession: JQ1315
A:Molecule type: genomic RNA
A:Residues: 1-157 <ALO>
A:Cross-references: UNIPROT:P29096; UNIPARC:UPI0000000361; GB:M81413; NID:g333293; PIDN:
A>Note: The authors translated the codon AAT for residue 26 as Ala, CAA for residue 46 ;
C:Superfamily: tobacco mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
Query Match 58.1%; Score 43; DB 1; Length 157;
Best Local Similarity 69.2%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 VENPMNRLVAETL 15
DB 97 VENPQNPTTAETL 109
|||||
RESULT 3
A87266
sensor histidine kinase/response regulator [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87266
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87266
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <STO>
A:Cross-references: UNIPROT:Q9ABT2; UNIPARC:UPI000000C6F46; GB:AE005673; NID:g13421249; I
C:Genetics:
A/Gene: CC0138
Query Match 55.4%; Score 41; DB 2; Length 514;
Best Local Similarity 57.1%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 AVENPMNRLVAETL 15
DB 385 AEDNPINALLIATL 398
|||||

JC6516
signal recognition particle protein Sec65 - yeast (*Yarrowia lipolytica*)
N:Alternate names: SRP19
C:Species: *Yarrowia lipolytica*, *Candida lipolytica*
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JG6516; S44157
R:Sanchez, M.; Beckerich, J.M.; Gallardin, C.; Dominguez, A.
Gene 203, 75-84, 1997
A:Title: Isolation and cloning of the *Yarrowia lipolytica* SEC65 gene, a component of the
A:Reference number: JC6516; MUID:98085978; PMID:9426009
A:Accession: JC6516
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <SAN>
A:Cross-references: UNIPROT:P41922; UNIPARC:UPI0000000313; EMBL:Z22570; NID:G473182; PID

Query Match 54.1%; Score 40; DB 2; Length 310;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AVENPMNRLVAE 13
Db 146 AVENPLGQTIAE 157
|||||: :|||

RESULT 5
E69878
RNA-binding Sun protein homolog ylom - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: E69878
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrtra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69878
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-447 <KUN>
A:Cross-references: UNIPROT:P94464; UNIPARC:UPI00000603AF; GB:Z99112; GB:AL009126; NID:G
A:Experimental source: strain 168
C:Genetics:
C:Gene: ylom
C:Superfamily: ribosomal RNA small subunit methyltransferase B

Query Match 54.1%; Score 40; DB 1; Length 447;
Best Local Similarity 53.8%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AVENPMNRLVAET 14
Db 136 AIEDPVRRLAET 148
|||||: :|||

RESULT 6
AH3098
rhizobium/RTX toxin [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AH3098
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH3098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1944 <KUR>
A:Cross-references: UNIPROT:Q8U7N7; UNIPARC:UPI0000164922; GB:AE008689; PIDN:AAL45206.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: rzca
A:Map position: linear chromosome

Query Match 54.1%; Score 40; DB 2; Length 1944;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 FAVENPMNRLVAETL 15
Db 255 FTVQSENKVVAAITL 269
|||||: :|||

RESULT 7
A96188
probable phosphoesterase (EC 3.1.1.-) yvnb [imported] - *Agrobacterium tumefaciens* (strain
C:Species: *Agrobacterium tumefaciens*
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A96188
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A96188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1990 <KUR>
A:Cross-references: UNIPROT:Q8U7N7; UNIPARC:UPI000000D256D; GB:AE007870; PIDN:AK89027.1;
C:Genetics:
A:Gene: agr L 909
A:Map position: linear chromosome

Query Match 54.1%; Score 40; DB 2; Length 1990;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 FAVENPMNRLVAETL 15
Db 301 FTVQSENKVVAAITL 315
|||||: :|||

RESULT 8
A60023
coat protein - *Odontoglossum ringspot virus*
C:Species: *Odontoglossum ringspot virus*
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A60023
R:Dubs, M.C.; van Regenmortel, M.H.V.
Arch. Virol. 115, 239-249, 1990
A:Title: *Odontoglossum ringspot virus* coat protein: sequence and antigenic comparisons
A:Reference number: A60023; MUID:91083518; PMID:2260922
A:Accession: A60023
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-158 <DUB>
A:Cross-references: UNIPROT:O12854; UNIPARC:UPI00000178706
C:Superfamily: tobacco mosaic virus coat protein

Query Match 52.7%; Score 39; DB 2; Length 158;

Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
|||||
DB 99 VENPQNPTTETL 111

RESULT 9
S14468
coat protein - odontoglossum ringspot virus
C/Species: odontoglossum ringspot virus
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S14468
R/Isomura, Y.; Matumoto, Y.; Murayama, A.; Chatani, M.; Inouye, N.; Ikegami, M.
submitted to the EMBL Data Library, October 1990
A/Description: Nucleotide sequence of coat protein gene of odontoglossum ringspot virus.
A/Reference number: S14468
A/Accession: S14468
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-158 <ISO>
A/Cross-references: UNIPROT:P03578; UNIPARC:UPI00001710C2; EMBL:X55295; NID:g62084; PIDN
C/Superfamily: tobacco mosaic virus coat protein

Query Match 52.7%; Score 39; DB 2; Length 158;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
|||||
DB 99 VENPQNPTTETL 111

RESULT 10
JQ1266
coat protein - odontoglossum ringspot virus
C/Species: odontoglossum ringspot virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JQ1266
R/Isomura, Y.; Matumoto, Y.; Murayama, A.; Chatani, M.; Inouye, N.; Ikegami, M.
J. Gen. Virol. 72, 2247-2249, 1991
A/Title: Molecular cloning, sequencing and expression in Escherichia coli of the odontog
A/Reference number: JQ1265; MUID:91374025; PMID:1895062
A/Accession: JQ1266
A/Molecule type: genomic RNA
A/Residues: 1-158 <ISO>
A/Cross-references: UNIPROT:P03578; UNIPARC:UPI0000178705
C/Genetics:
A/Introns: 304/3
C/Superfamily: tobacco mosaic virus coat protein

Query Match 52.7%; Score 39; DB 2; Length 158;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
|||||
DB 99 VENPQNPTTETL 111

RESULT 11
T02666
germin-like protein 16 - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02666
R/Yun, C.H.; Park, J.H.; Lee, J.H.; Eun, M.Y.
submitted to the EMBL Data Library, January 1998
A/Description: Nucleotide sequence of rice germin-like protein.
A/Reference number: Z14693
A/Accession: T02666
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-221 <YUN>
A/Cross-references: UNIPROT:O49181; UNIPARC:UPI00000A3D8D; EMBL:AF042489; NID:g2801802;
A/Experimental source: strain Nipponbare
C/Genetics:
A/Gene: glp16
C/Superfamily: germin

Query Match 52.7%; Score 39; DB 2; Length 221;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
|:|:|:|:|:|:|
DB 132 FVMSNPDNRLLSKVL 146

RESULT 12
JC5590
cycloartenol synthase (EC 5.4.99.8) - garden pea
C/Species: Pisum sativum (garden pea)
C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C/Accession: JC5590
R/Morita, M.; Shibuya, M.; Lee, M.S.; Sankawa, U.; Ebizuka, Y.
Biol. Pharm. Bull. 20, 770-775, 1997
A/Title: Molecular cloning of pea cDNA encoding cycloartenol synthase and its functional
A/Reference number: JC5590; MUID:97399291; PMID:9255418
A/Accession: JC5590
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-756 <MOR>
A/Cross-references: UNIPROT:O23909; UNIPARC:UPI00000AA343; GB:D89619; NID:g2627180; PIDN
C/Superfamily: yeast lanosterol synthase
C/Keywords: intramolecular transferase; isomerase

Query Match 52.7%; Score 39; DB 2; Length 756;
Best Local Similarity 63.6%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAVENPMNRLV 11
|||:|:|:|:|:|
DB 67 FAKENPMNEVL 77

RESULT 13
ISECTB
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Escherichia coli (strain K-
N/Alternate names: DNA gyrase B chain; type II DNA topoisomerase B chain
C/Species: Escherichia coli
C/Date: 30-Sep-1988 #sequence_revision 31-Oct-1997 #text_change 05-Oct-2004
C/Accession: D65172; A26444; A26953; C22168; A38344
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: D65172
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-804 <BLAT>
A/Cross-references: UNIPROT:P06982; UNIPARC:UPI0000168185; GB:AE000447; GB:U000096; NID:
A/Experimental source: strain K-12, substrain MG1655
R/Adachi, T.; Mizuuchi, M.; Robinson, E.A.; Appella, E.; O'Dea, M.H.; Gellert, M.; Mizu
Nucleic Acids Res. 15, 771-784, 1987
A/Title: DNA sequence of the E. coli gyrB gene: application of a new sequencing strateg
A/Reference number: A93674; MUID:87146392; PMID:3029692
A/Accession: A26444
A/Molecule type: DNA
A/Residues: 1-384, A', 386-804 <ADA>
A/Cross-references: UNIPARC:UPI000016552C; GB:X04341; GB:X00870; NID:g41643; PIDN:CAA27
R/Wenzel, R.; Gellert, M.
J. Bacteriol. 169, 1272-1278, 1987
A/Title: Fusions of the Escherichia coli gyrA and gyrB control regions to the galactoki

A:Reference number: A26953; MUID:87137287; PMID:3029031
 A:Accession: A26953
 A:Molecule type: DNA
 A:Residues: 1-23 <MEN>
 A:Cross-references: UNIPARC:UPI000016F1EF; GB:M15548; NID:gl146307; PIDN:AAA23949.1; PID:
 R:Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
 Nucleic Acids Res. 12, 6389-6395, 1984
 A:Title: DNA sequence and transcription of the region upstream of the E. coli gyrB gene.
 A:Reference number: A22168; MUID:84297235; PMID:6089112
 A:Accession: C22168
 A:Molecule type: DNA
 A:Residues: 1-50, 'R', 52-55, 'L', 57-106 <AD2>
 A:Cross-references: UNIPARC:UPI00001730B3
 R:Tamura, J.K.; Gellert, M.
 J. Biol. Chem. 265, 21342-21349, 1990
 A:Title: Characterization of the ATP binding site on Escherichia coli DNA gyrase. Affini
 A:Reference number: A38344; MUID:91065955; PMID:2174443
 A:Accession: A38344
 A:Molecule type: protein
 A:Residues: 93-126, 'X', 128-129 <TAM>
 A:Cross-references: UNIPARC:UPI00001730B4
 A:Note: Lys-103 and Lys-110 were shown to bind covalently to the ATP analog and DNA gyra
 C:Comment: DNA gyrase, which catalyzes DNA supercoiling and relaxing, is made up of two
 C:Genetics:
 A:Gene: gyrB
 A:Map position: 83 min
 A:Superfamily: Type II topoisomerase, subunit B
 C:Keywords: antibiotic resistance; ATP; DNA supercoiling; isomerase
 P:93-129/Region: ATP-binding

Query Match 52.7%; Score 39; DB 1; Length 804;

Best Local Similarity 64.3%; Pred. No. 89;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMNRLVAETL 15

||| ||| ||| ||| |||

Db 348 AVEQQMNEALLAYL 361

RESULT 14

DNA gyrase subunit B GyrB [imported] - Escherichia coli (strain O157:H7, substrain R1MD
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: B91208
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-804 <HAY>
 A:Cross-references: UNIPROT:P06982; UNIPARC:UPI000016552C; GB:BA000007; PIDN:BAB38057.1;
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: EC84634
 C:Superfamily: Type II topoisomerase, subunit B

Query Match 52.7%; Score 39; DB 2; Length 804;

Best Local Similarity 64.3%; Pred. No. 89;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMNRLVAETL 15

||| ||| ||| ||| |||

Db 348 AVEQQMNEALLAYL 361

RESULT 15

D86054
 hypothetical protein gyrB [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C:Accession: D86054
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: D86054
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-804 <STO>
 A:Cross-references: UNIPARC:UPI000016598B; GB:AE005174; NID:gl2518538; PIDN:AAG58896.1;
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: gyrB
 C:Superfamily: Type II topoisomerase, subunit B

Query Match 52.7%; Score 39; DB 2; Length 804;

Best Local Similarity 64.3%; Pred. No. 89;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMNRLVAETL 15

||| ||| ||| ||| |||

Db 348 AVEQQMNEALLAYL 361

RESULT 16

T02591

germin-like protein 3 - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C:Accession: T02591

R:Membre, N.; Bernier, F.

submitted to the EMBL Data Library, November 1997

A:Reference number: Z14634

A:Accession: T02591

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-181 <MEM>

A:Cross-references: UNIPROT:O48999; UNIPARC:UPI00000AB2D7; EMBL:AF032973; NID:G2655288;

C:Genetics:

A:Gene: GER3

C:Superfamily: germin

Query Match 51.4%; Score 38; DB 2; Length 181;

Best Local Similarity 46.7%; Pred. No. 25;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETL 15

||| ||| ||| ||| |||

Db 92 FVTSNPDNRLLSKVL 106

RESULT 17

T40694

probable rna maturation protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T40694

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.

submitted to the EMBL Data Library, February 1999

A:Reference number: Z21945

A:Accession: T40694

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-773 <WOO>

A:Cross-references: UNIPROT:O94689; UNIPARC:UPI000006BF80; EMBL:AL035536; PIDN:CAB36867;

A:Experimental source: strain 972h-; cosmid c83

C:Genetics:

A:Gene: SPDB:SPBC83.05

A:Map position: 2

C:Superfamily: Saccharomyces cerevisiae RNA12 protein

```

Query Match          51.4%; Score 38; DB 2; Length 773;
Best Local Similarity 63.6%; Pred. NO. 1.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3  VENNMRRLVAE 13
      : ||| ||| : |||
Db      480  LSNPMQRVAAE 490

RESULT 18
F83292
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: F83292
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
..J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: F83292
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-786 <STO>
A/Cross-references: UNIPROT:Q9T019; UNIPARC:UPI000000C582A; GB:AE004709; GB:AE004091; NID
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA2824

```

```

Query Match      51.4%; Score 38; DB 2; Length 786;
Best Local Similarity 55.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ENPMNRLVAETL 15
   :|:|:|:|:|
Db 670 DNPVNQLVAKGL 681

```

RESULT 19
H97798
hypothetical protein RC0792 [Imported] - Rickettsia conorii (strain Malish 7)
C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: H97798
C/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A/Reference number: A97700; MUID:21442074; PMID:11557893
A/Accession: H97798
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-50 <KUR>
A/Cross-references: UNIPROT:Q92HH9; UNIPARC:UPI00000CBED9; GB:AE006914; PIDN:AAL03330.1;A
C/Genetics:
A/Gene: RC0792

```

Query Match      50.0%; Score 37; DB 2; Length 50;
Best Local Similarity 46.2; Pred. No. 8.9;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 FAVENPMNRLVAE 13
      |||: |||:
Db      28 FIVQEPFNRIVCD 40

```

```

RESULT 20
A48418
interleukin-5 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A48418; S37641
R/Uberla, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein,

```

Cytokine 3, 72-81, 1991

A>Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A:Reference number: A48418; MUID:91355638; PMID:1653053
A:Accession: A48418
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <UBE>
A:Cross-references: UNIPROT:Q08125; UNIPARC:UPI000012D4D3; EMBL:X54419; NID:g3l3254; PII
A:Experimental source: cell line TR5-1
A>Note: sequence extracted from NCBI backbone (NCBIN:63651, NCBI:P:63652)
C:Superfamily: interleukin-5
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-132/Product: interleukin-5 #status predicted <MAT>
F:45-74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:61/Disulfide bonds: interchain (to 103) #status predicted
F:103/Disulfide bonds: interchain (to 61) #status predicted

Query Match	50.0%;	Score 37;	DB 1;	Length 132;
Best Local Similarity	57.1%;	Pred. No. 27;		
Matches	8;	Conservative	3;	Mismatches
			3;	Indels
				Gaps
				0;

Qy 2 AVENPMNRLVAETL 15
 | : | | : | | |
Db 19 AMEIPMTSTWVKETL 32

RESULT 21
ICMS5
interleukin-5 precursor - mouse
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil c
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C:Accession: S00807; A38758; A24898; J50077; PH0102; B39881
R:Campbell, H.D.; Sanderson, C.J.; Wang, Y.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.;
Eur. J. Biochem. 174, 345-352, 1988
A:Title: Isolation, structure and expression of cDNA and genomic clones for murine eosin
n-5.

A;Reference number: S00807; NCID:306254002; PMID:3333200
A;Accession: S00807
A;Molecule type: DNA
A;Residues: 1-133 <CAM>
A;Cross-references: UNIPROT:P04401; UNIPARC:UPI0000026C25; EMBL:X06271; NID:G52685; PIDN:PIDN
A;Accession: A38758
A;Molecule type: mRNA
A;Residues: 1-133 <CAM2>
A;Cross-references: UNIPARC:UPI0000026C25; EMBL:X06270; NID:G52687; PIDN:CAA29506.1; PII:PII
R;Kinashi, T.; Harada, N.; Severinsson, B.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma, M.;
Nature 324, 70-73, 1986
A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
A;Reference number: A24898; MUID:87065032; PMID:3024009
A;Accession: A24898
A;Molecule type: mRNA
A;Residues: 1-133 <KIN>
A;Cross-references: UNIPARC:UPI0000026C25; EMBL:X04601; NID:G54998; PIDN:CAA28266.1; PII:PII
R;Miura, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: D71206

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-162 <KAW>

A;Cross-references: UNIPROT:O59581; UNIPARC:UPI0000063178; GB:AP000007; NID:G3236134; P1

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1918

C;Superfamily: hypothetical protein MTH699

Query Match 50.0%; Score 37; DB 1; Length 162;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMNRLVAET 14
| | | | : | | |
Db 111 ASENPFQVIVAET 123

RESULT 24

H75019

hypothetical protein PAB1234 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: H75019

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Accession: H75019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-162 <KAW>

A;Cross-references: UNIPROT:Q9UY14; UNIPARC:UPI00000634BB; GB:AJ248288; GB:AL096836; NID

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB1234

C;Superfamily: hypothetical protein MTH699

Query Match 50.0%; Score 37; DB 2; Length 162;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AVENPMNRLVAET 14
| | | | : | | |
Db 111 ASENPFQVIVAET 123

RESULT 25

E85565

probable trna synthetase ybeK [imported] - Escherichia coli (strain O157:H7, substrain F

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: E85565

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E85565

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-311 <STO>

A;Cross-references: UNIPROT:Q8XBL8; UNIPARC:UPI0000000597; GB:AE005174; NID:G12513558; P

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: ybeK

C;Superfamily: yaaF protein

Query Match 50.0%; Score 37; DB 2; Length 311;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
 : : : : :
 Db 207 AIGNPVSTIVAE LL 220

RESULT 26
 B30715
 probable tRNA synthetase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: B30715
 R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasavara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A39629; MUID:21156231; PMID:11258796
 A:Accession: B30715
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-311 <HAV>
 A:CROSS-references: UNIPROT:Q8XBL8; UNIPARC:UPI00000D0597; GB:BA000007; PIDN:BA034113.1;
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 C:Superfamily: yaaF protein

Query Match 50.0%; Score 37; DB 2; Length 311;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
 : : : : :
 Db 207 AIGNPVSTIVAE LL 220

RESULT 27
 A64800
 purine nucleosidase-related protein ybek - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: A64800
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: A64800
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-311 <BLAT>
 A:CROSS-references: UNIPROT:P41409; UNIPARC:UPI000013A301; GB:AE000169; GB:U00096; NID:9
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ybek
 C:Superfamily: yaaF protein
 C:Keywords: transmembrane protein
 F:17-33/Domain: transmembrane #status predicted <TM>

Query Match 50.0%; Score 37; DB 2; Length 311;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
 : : : : :
 Db 207 AIGNPVSTIVAE LL 220

RESULT 28
 B42519

A18R protein - vaccinia virus (strain Copenhagen)
 C:Species: vaccinia virus
 A>Note: host Homo sapiens (man)
 C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
 C:Accession: B42519
 R:Johnson, G.P.
 submitted to GenBank, June 1990
 A:Reference number: A33172
 A:Accession: B42519
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-493 <JOH>
 A:CROSS-references: UNIPROT:P20534; UNIPARC:UPI0000013804F

Query Match 50.0%; Score 37; DB 2; Length 493;
 Best Local Similarity 42.9%; Pred. No. 1.2e+02;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
 : : : : :
 Db 300 SVDEPRNQLIDTL 313

RESULT 29
 S23429
 protein kinase ERK3 (EC 2.7.1.1.-) - human
 N:Alternate names: extracellular signal-regulated kinase 3; protein kinase, 63K
 C:Species: Homo sapiens (man)
 C>Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
 C:Accession: S23429; S21580
 R:Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
 PDBS Lett. 304, 170-178, 1992
 A>Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
 A:Reference number: S23426; MUID:92316223; PMID:1319925
 A:Accession: S23429
 A:Molecule type: mRNA
 A:Residues: 1-557 <GON>
 A:CROSS-references: UNIPROT:P31152; UNIPARC:UPI000012F175; EMBL:X59727; NID:G23902; PIDN:529

C:Genetics:
 A:Gene: GDB:PRK4; MAPK4; ERK3
 A:CROSS-references: GDB:135680; OMIM:176949
 A:Map position: 18q12-18q21
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:18-281/Domain: protein kinase homology <KIN>
 F:26-34/Region: protein kinase ATP-binding motif

Query Match 50.0%; Score 37; DB 2; Length 557;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 NPMNRLVAE 13
 : : : : :
 Db 296 NPMNRLTAE 304

RESULT 30
 T41681
 probable serine/threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41681
 R:Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z21742
 A:Accession: T41681
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-650 <WED>
 A:CROSS-references: UNIPROT:Q9U085; UNIPARC:UPI00000697F2; EMBL:AL117183; PIDN:CAB54861
 A:Experimental source: strain 972h-; clone pl p1E11
 C:Genetics:
 A:Gene: SPDB:SPCP1E11.02
 A:Map position: 3

A: Introns: 42/1; 85/3; 235/1
C: Superfamily: yeast hypothetical protein YNL020c; protein kinase homology

Query Match 50.0%; Score 37; DB 2; Length 650;
Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAET 14
: ||||| :
Db 533 SVENPQNNISAPT 545

Search completed: December 17, 2005, 07:33:37
Job time : 42 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2005, 07:21:22 ; Search time 226 Seconds
(without alignments)
46.827 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74

Sequence: 1 FAVENPMRLVAETL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	74	100.0	118	QFTV10_CANFA	Q9cv10 canis famil
2	74	100.0	134	I1L5_CANFA	Q95j76 canis famil
3	63	85.1	134	I1L5_HORSE	O02699 equus cabal
4	60	81.1	134	I1L5_FELCA	O77515 felis silve
5	60	81.1	134	Q9MYM5_PIG	Q9mym5 sus scrofa
6	60	81.1	134	Q9TSD7_FELCA	Q9tsd7 felis silve
7	55	74.3	132	I1L5_SHEEP	Q28586 ovis aries
8	55	74.3	134	I1L5_BOVIN	P52173 bos taurus
9	47	63.5	696	Q9KYA5_STRCO	Q9kyas streptomyce
10	46	62.2	132	I1L5_SIGHI	Q9sei9 sigmodon hi
11	46	62.2	457	Q846W1_STRCM	Q846w1 streptomyce
12	44	59.5	139	I1L5_MACEU	Q9xt91 macropus eu
13	44	59.5	419	O08402_9ENTR	O08402 citrobacter
14	43	58.1	156	1 COAT_PMMV2	Q9wdg5 pepper mild
15	43	58.1	156	1 COAT_PMMV1	Q84843 pepper mild
16	43	58.1	156	1 COAT_PMMVJ	P69509 pepper mild
17	43	58.1	156	1 COAT_PMMVS	P69510 pepper mild
18	43	58.1	156	1 COAT_TOMKO	Q83482 tobacco mos
19	43	58.1	157	2 Q6LRI3_9VIRU	Q6lri3 tobacco mos
20	43	58.1	157	2 Q76M57_9VIRU	Q76m57 pepper mild
21	43	58.1	157	2 Q780A7_9VIRU	Q780a7 pepper mild
22	43	58.1	157	2 Q80P27_9VIRU	Q80p27 pepper mild
23	43	58.1	157	2 Q81E32_9VIRU	Q81e32 pepper mild
24	43	58.1	157	2 Q81U97_9VIRU	Q81u97 pepper mild
25	43	58.1	157	2 Q91U98_9VIRU	Q91u98 pepper mild
26	43	58.1	157	2 Q91U99_9VIRU	Q91u99 pepper mild
27	43	58.1	157	2 Q91UA0_9VIRU	Q91ua0 pepper mild
28	43	58.1	157	2 Q91UA1_9VIRU	Q91ua1 pepper mild
29	43	58.1	158	1 COAT_PMMV0	Q9wdg3 pepper mild
30	43	58.1	158	2 Q83483_9VIRU	Q83483 tobacco mos
31	43	58.1	160	2 Q4VFY0_9VIRU	Q4vfy0 tropical so

32	43	58.1	257	2	Q4LQM7_9BURK	Q4lqm7 burkholderi
33	43	58.1	2679	2	Q60PH9_CAEBR	Q60ph9 caenorhabdi
34	42	56.8	109	2	Q4YST9_PLABE	Q4yst9 plasmodium
35	42	56.8	222	1	GL19_ARATH	Q9fmb0 arabidopsis
36	42	56.8	1088	2	G52G72_MAGGR	Q52g72 magnaporthe
37	41	55.4	164	2	Q94SD6_CASSA	Q94sd6 castanea sa
38	41	55.4	307	2	Q9VJ85_DROME	Q9vj85 drosophila
39	41	55.4	320	2	Q8INX3_DROME	Q8inx3 drosophila
40	41	55.4	514	2	Q9ABT2_CAUCR	Q9abt2 caulobacter
41	41	55.4	583	2	Q8ZMS8_SALTY	Q8zms8 salmomella
42	41	55.4	602	2	Q8F5P8_LEPIN	Q8f5p8 leptospira
43	41	55.4	602	2	Q72O59_LEPIC	Q72o59 leptospira
44	41	55.4	866	2	Q623F4_CAEBR	Q623f4 caenorhabdi
45	40	54.1	90	2	Q7Y520_BPR69	Q7y520 bacterioph
46	40	54.1	252	2	Q6HMY5_BACHK	Q6hmy5 bacillus th
47	40	54.1	310	1	SEC65_YARLI	P41922 yarrowia li
48	40	54.1	315	2	Q9R9L5_RHIME	P41922 yarrowia li
49	40	54.1	315	2	Q9X983_RHIME	Q9x983 rhizobium m
50	40	54.1	345	2	Q8GRD4_SSP10	Q8grd4 bradyrhizob
51	40	54.1	351	2	Q89FF6_BRAJA	Q89ff6 bradyrhizob
52	40	54.1	383	2	Q5SLZ6_CRYNE	Q5slz6 cryptococcu
53	40	54.1	383	2	Q5K8S2_CRYNE	Q5k8s2 cryptococcu
54	40	54.1	405	2	Q8D4F3_VIBVU	Q8d4f3 vibrio vuln
55	40	54.1	435	2	Q7MFY2_VIBVY	Q7mfy2 vibrio vuln
56	40	54.1	447	1	RSMB_BACSU	P94464 bacillus su
57	40	54.1	502	2	Q988B0_RHILO	Q988b0 rhizobium l
58	40	54.1	759	2	Q4XZV6_PLACH	Q4xzv6 plasmodium
59	40	54.1	761	2	Q4YNR3_PLABE	Q4ynr3 plasmodium
60	40	54.1	771	2	Q7RNA9_PLAYO	Q7rna9 plasmodium
61	40	54.1	862	2	Q8IL36_PLAF7	Q8il36 plasmodium
62	40	54.1	1944	2	Q8U7N7_AGR75	Q8u7n7 agrobacteri
63	40	54.1	1952	2	Q6LXQ2_CAEBR	Q6lqx2 caenorhabdi
64	40	54.1	1990	2	Q7CUW1_AGR75	Q7cuw1 agrobacteri
65	40	54.1	4915	2	Q6CJB6_KULUA	Q6cjb6 kluyveromyc
66	39	52.7	147	2	Q7QSS7_GIALA	Q7qss7 giardia lam
67	39	52.7	147	2	Q8T4N8_GIALA	Q8t4n8 giardia lam
68	39	52.7	149	2	Q8VL28_ECOLI	Q8vl28 escherichia
69	39	52.7	157	1	COAT_ORSVJ	P03578 odontogloss
70	39	52.7	157	1	COAT_ORSVS	Q84136 odontogloss
71	39	52.7	157	2	Q76U57_9VIRU	Q76u57 odontogloss
72	39	52.7	158	2	Q5K647_9VIRU	Q5k647 odontogloss
73	39	52.7	158	2	Q5K648_9VIRU	Q5k648 odontogloss
74	39	52.7	158	2	Q5K6A9_9VIRU	Q5k6a9 odontogloss
75	39	52.7	158	2	Q5K6B1_9VIRU	Q5k6b1 odontogloss
76	39	52.7	158	2	Q5K6B3_9VIRU	Q5k6b3 odontogloss
77	39	52.7	158	2	Q5K6B6_9VIRU	Q5k6b6 odontogloss
78	39	52.7	158	2	Q5K6C1_9VIRU	Q5k6c1 odontogloss
79	39	52.7	158	2	Q5TUK4_9VIRU	Q5tjk4 odontogloss
80	39	52.7	158	2	Q5TUK5_9VIRU	Q5tjk5 odontogloss
81	39	52.7	158	2	Q80P28_9VIRU	Q80p28 odontogloss
82	39	52.7	158	2	Q80P29_9VIRU	Q80p29 odontogloss
83	39	52.7	158	2	Q80P30_9VIRU	Q80p30 odontogloss
84	39	52.7	158	2	O12854_9VIRU	O12854 odontogloss
85	39	52.7	172	2	Q6W159_RHISN	Q6w159 rhizobium s
86	39	52.7	180	2	Q9U249_CABEL	Q9u249 caenorhabdi
87	39	52.7	221	2	Q49181_ORYSA	Q49181 oryza sativ
88	39	52.7	252	2	Q81HD1_BACCR	Q81hd1 bacillus ce
89	39	52.7	278	2	Q6MAX1_PARUW	Q6max1 parachlamyd
90	39	52.7	323	2	Q937H5_HAFAL	Q937h5 hafnia alve
91	39	52.7	364	2	Q4UPL9_XANCP	Q4upl9 xanthomonas
92	39	52.7	364	2	Q8P437_XANCP	Q8p437 xanthomonas
93	39	52.7	369	2	Q754V8_ASHGO	Q754v8 ashbya goss
94	39	52.7	390	2	Q8LOR2_ECOLI	Q8lor2 escherichia
95	39	52.7	390	2	Q8LOR3_ECOLI	Q8lor3 escherichia
96	39	52.7	390	2	Q8LOR1_ECOLI	Q8lor1 escherichia
97	39	52.7	390	2	Q8LOR4_ECOLI	Q8lor4 escherichia
98	39	52.7	390	2	Q8KHV8_ECOLI	Q8khv8 escherichia
99	39	52.7	390	2	Q8KIA4_ECOLI	Q8kia4 escherichia
100	39	52.7	390	2	Q8KIA0_SHISO	Q8kia0 shigella so
101	39	52.7	390	2	Q8KIA1_SHIFO	Q8kia1 shigella fl
102	39	52.7	390	2	Q8KIA2_SHIBO	Q8kia2 shigella bo
103	39	52.7	390	2	Q8KIA3_ECOLI	Q8kia3 escherichia
104	39	52.7	408	2	Q70GL9_RETFI	Q70gl9 reticulomyc

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105 39 52.7 502 2 Q5YUM9 NOCFA
106 39 52.7 518 2 Q9VF72 DROME
107 39 52.7 576 2 Q5CN36 CRYHO
108 39 52.7 586 2 Q5CYA3 CRYPV
109 39 52.7 692 2 Q98AD7 RHIZO1
110 39 52.7 756 2 Q23909 PEA
111 39 52.7 757 2 Q9SKV6 GLYGL
112 39 52.7 803 1 GYRB EGOLI
113 39 52.7 805 2 Q8FV7 ECOL6
114 39 52.7 829 2 Q4PD86 USTLAGO
115 39 52.7 832 2 Q7YYP6 CRYPV
116 39 52.7 844 2 Q5CWS4 CRYPV
117 39 52.7 949 2 Q5B169 EMENI
118 39 52.7 1104 2 Q75F16 ASHGO
119 38.5 52.0 234 2 Q80LP5 NPVAH
120 38.5 52.0 717 2 Q87J33 NEURP
121 38 51.4 85 2 Q93EH8 HELHP
122 38 51.4 135 2 Q6NKC1 CORDI
123 38 51.4 181 2 Q48999 ORYSA
124 38 51.4 221 2 Q6YZA8 ORYSA
125 38 51.4 223 2 Q6QGH8 XENLA
126 38 51.4 235 2 Q9KX14 RHODOB
127 38 51.4 252 2 Q4MWH7 BACCE
128 38 51.4 252 2 Q73CV7 BACCI
129 38 51.4 252 2 Q81UK1 BACAN
130 38 51.4 274 2 Q62D39 BURMA
131 38 51.4 274 2 Q63M77 BURPS
132 38 51.4 344 2 Q75DGI ASHGO
133 38 51.4 401 2 Q82NG0 STRAW
134 38 51.4 471 1 TYPH MOUSE
135 38 51.4 521 2 Q7VJ33 HELHP
136 38 51.4 528 2 Q8G9V8 ECOLI
137 38 51.4 538 2 Q5P5Q6 AZOSE
138 38 51.4 617 2 Q6M987 NEURP
139 38 51.4 623 2 Q6S7E9 MOUSE
140 38 51.4 631 2 Q65M44 BACLD
141 38 51.4 714 2 Q7SA10 NEURC
142 38 51.4 721 2 Q511J9 ENTHI
143 38 51.4 728 2 Q6MYU3 ASPFU
144 38 51.4 766 2 Q4WSR2 ASPFU
145 38 51.4 773 2 Q94689 SCHPO
146 38 51.4 786 2 Q91019 PSEDO
147 38 51.4 923 2 Q4J1A7 AZOVI
148 38 51.4 937 2 Q82Z87 ENTHI
149 38 51.4 939 2 Q4WXJ6 ASPFU
150 38 51.4 1041 2 Q8L816 CATRO

```

ALIGNMENTS

```

RESULT 1
ID Q9TV10 CANFA PRELIMINARY; PRT; 118 AA.
AC Q9TV10
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC EMBL; AF091133; AAD46991.1; -; mRNA.

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DR HSSP; P05113; 1HUL.
DR Ensembl; ENSCAFG0000000855; Canis familiaris.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;
Query Match 100.0%; Score 74; DB 2; Length 118;
Best Local Similarity 100.0%; Pred.No. 5.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMNRLVAETL 15
Db 8 FAVENPMNRLVAETL 22
RESULT 2
ID IL5 CANFA STANDARD; PRT; 134 AA.
AC Q95J76
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name=IL5;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=23334408; PubMed=11440633; DOI=10.1089/107999001750277835;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT "Canine interleukin-5: molecular characterization of the gene and
RT expression of biologically active recombinant protein.";
RL J. Interferon Cytokine Res. 21:361-367(2001).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF331920; AAL10716.1; -; Genomic_DNA.
CC EMBL; AF331919; AAL10715.1; -; mRNA.
CC HSSP; P05113; 1HUL.
CC Ensembl; ENSCAFG0000000855; Canis familiaris.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC InterPro; IPR000186; Interleukin_5.
CC PANTHER; PTHR10525; Interleukin_5; 1.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 134 Interleukin-5.
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT DISULFID 63 63 Interchain (with C-105) (By similarity).

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FT DISULFID 105 105 Interchain (with C-63) (By similarity).
SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6F4C6 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.2e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 FAVENPMNRLVAETL 15
Db 20 FAVENPMNRLVAETL 34
|||||
|||||

RESULT 3
IL5_HORSE
ID IL5_HORSE STANDARD; PRT; 134 AA.
AC 002699;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name=IL5;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Vandersgrift E.V., Horobov D.W.;
RT "Equine interleukin-5.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U91947; AAB51382.1; -; mRNA.
CC SMR; 002699; 25-130.
CC InterPro; IPR012351; Cytokine 4 hlx.
CC InterPro; IPR000186; Interleukin_5.
CC PANTHER; PTHR10525; Interleukin_5; 1.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT PRODOM; PD006721; Interleukin_5; 1.
FT Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
SQ SEQUENCE 134 AA; 15081 MW; 2914840E3E7A006D CRC64;

Query Match 85.1%; Score 63; DB 1; Length 134;
Best Local Similarity 92.9%; Pred. No. 0.0057; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 1;

QY 2 AVENPMNRLVAETL 15
Db 21 AVESPMNRLVAETL 34
|||||
|||||

RESULT 4
IL5_FELCA

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ID IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name=IL5;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98452719; PubMed=9781459;
RA Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 12-128.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbour D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF025436; AAC64505.1; -; mRNA.
CC EMBL; AF051372; AAC05752.1; -; mRNA.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR012351; Cytokine 4 hlx.
CC InterPro; IPR000186; Interleukin_5.
CC PANTHER; PTHR10525; Interleukin_5; 1.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT DISULFID 63 63 Interchain (with C-105) (By similarity).
FT DISULFID 105 105 Interchain (with C-63) (By similarity).
FT CONFLICT 104 105 KC -> NF (in Ref. 2).
FT CONFLICT 108 111 ERWR -> KKWK (in Ref. 2).
FT CONFLICT 114 114 K -> N (in Ref. 2).
FT CONFLICT 117 117 D -> N (in Ref. 2).
FT CONFLICT 121 121 V -> F (in Ref. 2).
FT CONFLICT 125 126 VI -> LL (in Ref. 2).
SQ SEQUENCE 134 AA; 15224 MW; 87D18DB8F8C820 CRC64;

Query Match 81.1%; Score 60; DB 1; Length 134;
Best Local Similarity 85.7%; Pred. No. 0.02; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2;

QY 2 AVENPMNRLVAETL 15
Db 21 AVQSPMNLVAETL 34
|||||
|||||

RESULT 5
Q9MYM5_PIG
ID Q9MYM5_PIG PRELIMINARY; PRT; 134 AA.
AC Q9MYM5;

```

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Interleukin-5.
 GB Name=IL-5;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE 20130134; PubMed=10663563; DOI=10.1007/s002510050009;
 RA Sylvain H., Matvienko O., Leonchiks A., Aiving K., van der Plieg I.;
 RT "Molecular cloning, expression, and purification of pig interleukin-5";
 RL Immunogenetics 51:59-64(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
 RA Heegaard P.M.H.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AJ010088; CAB70611.2; -; mRNA.
 DR EMBL; AJ133452; CAB38328.1; -; mRNA.
 DR HSSP; P05113; 1HUL.
 DR SMR; Q9NVM5; 29-130.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PD00432; INTERLEUKINS.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Growth factor.
 SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;
 Query Match 81.1%; Score 60; DB 2; Length 134;
 Best Local Similarity 92.9%; Pred.No. 0.02; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;
 QY 2 AVENPMNRLVAETL 15
 DB 21 AVENTMNLVAETL 34
 RESULT 6
 ID Q9TSD7_FELCA PRELIMINARY; PRT; 134 AA.
 AC Q9TSD7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 5.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Vandegeft E., Hughes K.J., O'Reilly K.L.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AF068770; AAC27616.1; -; mRNA.
 DR HSSP; P05113; 1HUL.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PD00432; INTERLEUKINS.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Growth factor.
 SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8C820 CRC64;
 Query Match 81.1%; Score 60; DB 2; Length 134;
 Best Local Similarity 85.7%; Pred.No. 0.02; Mismatches 2; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Indels 0; Gaps 0;
 QY 2 AVENPMNRLVAETL 15
 DB 21 AVQSPMNLVAETL 34
 RESULT 7
 ID IL5_SHEEP STANDARD; PRT; 132 AA.
 AC Q28586;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN Name=IL5;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Seow H.-P., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
 RT "Cloning of ovine interleukin-5 cDNA";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 DR EMBL; U17053; AAB60629.1; -; Genomic DNA.
 DR EMBL; U17052; AAB60629.1; JOINED; Genomic DNA.
 DR EMBL; U35038; AAC59991.1; -; mRNA.
 DR HSSP; P05113; 1HUL.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000186; Interleukin_5.
 DR PANTHER; PTHR10525; Interleukin_5; 1.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKINS.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 132 Interleukin-5.

FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
 FT DISULFID 61 61 Interchain (with C-103) (By similarity).
 FT DISULFID 103 103 Interchain (with C-61) (By similarity).
 SQ SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;

Query Match 74.3%; Score 55; DB 1; Length 132;
 Best Local Similarity 85.7%; Pred. No. 0.15;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
 DB 19 AVESWNRRLVAETL 32

RESULT 8

IL5_BOVIN STANDARD; PRT; 134 AA.
 AC P52173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN Name=IL5;
 OS Bos taurus (Bovina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=97075944; PubMed=8918267; DOI=10.1016/0378-1119(96)00252-1;
 RA Mertens B., Gibrig E., Seow H.F.;
 RT "The nucleotide sequence of the bovine interleukin-5-encoding cDNA";
 RL Gene 176:273-274 (1996).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-developing B-cells to immunoglobulin secreting cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.

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 DR EMBL; Z67872; CAA91779.1; -; mRNA.
 DR PIR; JC5116; JC5116.
 DR HSP; P05113; 1HUL.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000186; Interleukin_5.
 DR PANTHER; PTHR10525; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKIN5.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 134 Interleukin-5.
 FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
 FT DISULFID 63 63 Interchain (with C-105) (By similarity).
 FT DISULFID 105 105 Interchain (with C-63) (By similarity).
 SQ SEQUENCE 134 AA; 15229 MW; 0B3A2328EE7431F4 CRC64;

Query Match 74.3%; Score 55; DB 1; Length 134;
 Best Local Similarity 85.7%; Pred. No. 0.15;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15

DB 21 AVESWNRRLVAETL 34

RESULT 9

Q9KYA5_STRCO PRELIMINARY; PRT; 696 AA.
 AC Q9KYA5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative O-methyltransferase.
 GN OrderedlocusNames=SCO6928; ORFNames=SC1B2.34c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Lark L., Murphy L.D., Oliver K., O'Neill S., Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.;
 RA "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
 RT Nature 417:141-147 (2002).
 RL EMBL; AL939129; CAB92590.1; -; Genomic_DNA.
 DR HSP; Q872R3; 1JGL.
 DR GO; GO:0004719; P:protein-L-isopartate (D-aspartate) O-meth. .; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006464; P:protein modification; IEA.
 DR InterPro; IPR000682; PCWT.
 DR InterPro; IPR000051; SAM_bind.
 DR Pfam; PF01135; PCMT; 1.
 DR Complete proteome; Methyltransferase; Transferase.
 KW SEQUENCE 696 AA; 75886 MW; 5C08C043308CFCBA CRC64;

Query Match 63.5%; Score 47; DB 2; Length 696;
 Best Local Similarity 61.5%; Pred. No. 23;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAR 13
 DB 682 FAFONPLNRVIE 694

RESULT 10

IL5_SIGHI STANDARD; PRT; 132 AA.
 AC Q985I9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN Name=IL5;
 OS Sigmodon hispidus (Hispid cotton rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetidae; Sigmodontinae; Sigmodon.
 OX NCBI_TaxID=42415;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX PubMed=11054577; DOI=10.1016/S0378-1119(00)00366-8;
 RA Houard S., Jacquet A., Haumont M., Damint V., Milican F., Glineur F.,

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RA Bollen A.;
RT "Cloning, expression and purification of recombinant cotton rat
RL Interleukin-5"; (2000).
CC Gene 257:149-155 (2000).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF148211; AAG16722.1; -; mRNA.
CC HSSP; P05113; 1HUL.
CC SMR; Q98S19; 22-128.
CC InterPro; IPR012351; Cytokine 4 hlx.
CC InterPro; IPR000186; Interleukin_5.
CC PANTHER; PTHR10525; Interleukin_5; 1.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 132 Interleukin-5.
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 74 74 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT DISULFID 61 61 Interchain (with C-103) (By similarity).
FT DISULFID 103 103 Interchain (with C-61) (By similarity).
SQ SEQUENCE 132 AA; 15434 MW; B328B81B2371FBB9 CRC64;

Query Match 62.2%; Score 46; DB 1; Length 132;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETL 15
DB 18 FAVEIPMHTVVKETL 32
|||||:|:|:|

RESULT 11
Q846W1_STRCM
ID Q846W1_STRCM PRELIMINARY; PRT; 457 AA.
AC Q846W1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Streptomyces cinnamonensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC15413;
RX MEDLINE=22823264; PubMed=12940979;
RX DOI=10.1046/j.1365-2958.2003.03571.x;
RA Olinnyk M., Stark C.B.W., Bhatt A., Jones M.A., Hughes-Thomas Z.A.,
RA Wilkinson C., Olinnyk Z., Demychuk Y., Scaunton J., Leadlay P.F.;
RA "Analysis of the biosynthetic gene cluster for the polyether
RT antibiotic monensin in Streptomyces cinnamonensis and evidence for the
RT role of monB and monC genes in oxidative cyclization.";
RL Mol. Microbiol. 49:1179-1190(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC15413;
RA Olinnyk M.;
RT "The gene cluster for monensin biosynthesis.";
RL Thesis (1999), University of Cambridge.
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DR EMBL; AF440781; AA065811.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 457 AA; 50456 MW; 9D53DB3362009F54 CRC64;

Query Match 62.2%; Score 46; DB 2; Length 457;
Best Local Similarity 69.2%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAE 13
DB 191 FSVHEPMSRLVAE 203
|:|:|:|:|:|:|

RESULT 12
IL5_MACEU
ID IL5_MACEU STANDARD; PRT; 139 AA.
AC Q9XT91;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
DE Name=IL5;
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99432005; PubMed=10501836; DOI=10.1007/s002510050577;
RA Hawken R.J., Maccarone P., Toder R., Marshall Graves J.A.,
RA Maddox J.P.;
RT "Isolation and characterization of marsupial IL5 genes.";
RL Immunogenetics 49:942-948(1999).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF064209; RAD37462.1; -; Genomic_DNA.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR012351; Cytokine 4 hlx.
CC InterPro; IPR000186; Interleukin_5.
CC PANTHER; PTHR10525; Interleukin_5; 1.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 139 Interleukin-5.
FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).
FT DISULFID 64 64 Interchain (with C-106) (By similarity).
FT DISULFID 106 106 Interchain (with C-64) (By similarity).
SQ SEQUENCE 139 AA; 15784 MW; CE16342A68F10622 CRC64;

Query Match 59.5%; Score 44; DB 1; Length 139;
Best Local Similarity 64.3%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AVENPMNRLVAETL 15
DB 22 ATGPNVSRSLVTETL 35
|:|:|:|:|:|
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RESULT 13
O08402_9ENTR PRELIMINARY; PRT; 419 AA.
ID O08402_9ENTR PRELIMINARY; PRT; 419 AA.
AC O08402_009479;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE DNA gyrase beta-subunit (Fragment).
GN Name=gyrB;
OS Citrobacter sp. JYME-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=60487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JYME-1;
RA Venkateswaran K., Nealeon K.H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AF005700; AAB80843.1; -; Genomic_DNA.
DR HSSP; P06982; IE11.
DR SMR; O08402; 1-286.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR011558; DNA gyrase_B.
DR InterPro; IPR001241; DNA topoisom.
DR InterPro; IPR000565; DNA topoisom IV_B.
DR Pfam; PF00204; DNA gyraseB; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 419
SQ SEQUENCE 419 AA; 46232 MW; E442532D303FDA52 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 419;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 AVENPMNRLVAETL 15
||| ||| :|||
Db 257 AVEQPMNLLSEYL 270

RESULT 14
COAT PMMV2
ID COAT PMMV2 STANDARD; PRT; 156 AA.
AC Q9WDG5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Coat protein.
GN Name=CP;
OS Pepper mild mottle virus (strain P2) (PMNV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=138305;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Sohn S.-H., Hahn J.-H., Hwang Y.-S.;
RT "The coat protein gene of Pepper Mild Mottle Virus isolated from Hot pepper in Korea".
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the tobamoviruses coat protein family.
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OY 3 VENPMNRLVAETL 15
||| | |||
Db 96 VENQNPPTAETL 108

Query Match 58.1%; Score 43; DB 1; Length 156;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 VENPMNRLVAETL 15
||| | |||
Db 96 VENQNPPTAETL 108

RESULT 16
COAT PMMVJ
ID COAT PMMVJ STANDARD; PRT; 156 AA.
AC P69509; P29096;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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CC EMBL; AF103778; AAD20289.1; -; mRNA.
DR HSSP; P03579; 1VTM.
DR InterPro; IPR001337; TMV coat.
DR Pfam; PF00721; TMV coat; 1.
KW Acetylation; Capsid protein; Structural protein.
FT INIT_MET 0
FT MOD_RES 1 N-acetylalanine (By similarity).
SQ SEQUENCE 156 AA; 17125 MW; ECD6A3A3D176A919 CRC64;

Query Match 58.1%; Score 43; DB 1; Length 156;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 VENPMNRLVAETL 15
||| | |||
Db 96 VENQNPPTAETL 108

RESULT 15
COAT PMMVI
ID COAT PMMVI STANDARD; PRT; 156 AA.
AC Q84843;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Coat protein.
GN Name=CP;
OS Pepper mild mottle virus (strain Italian) (PMMV-I).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=138306;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RA Garcia-Luque I., Ferrero M.L., Rodriguez J.M., Alonso E., de la Cruz A., Sanz A.I., Vaquero C., Serra M.T., Diaz-Ruiz J.R.;
RT "The nucleotide sequence of the coat protein genes and 3' non-coding regions of two resistance-breaking tobamoviruses in pepper shows that they are different viruses.";
RL Arch. Virol. 131:75-88(1993).
CC -!- SIMILARITY: Belongs to the tobamoviruses coat protein family.
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OY 3 VENPMNRLVAETL 15
||| | |||
Db 96 VENQNPPTAETL 108

Query Match 58.1%; Score 43; DB 1; Length 156;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 VENPMNRLVAETL 15
||| | |||
Db 96 VENQNPPTAETL 108

RESULT 16
COAT PMMVJ
ID COAT PMMVJ STANDARD; PRT; 156 AA.
AC P69509; P29096;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Coat protein.
 GN Name=CP;
 OS Pepper mild mottle virus (strain Japan) (PMMV-J).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OC NCBI_TaxID=138663;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Kirita M., Akutsu K., Watanabe Y., Tsuda S.;
 RT "Nucleotide sequence of the Japanese isolate of pepper [Capsicum
 annuum] mild mottle tobamovirus (TMV-P) RNA.";
 RL Ann. Phytopathol. Soc. Jpn. 63:373-376(1997).
 CC -!- SIMILARITY: Belongs to the tobamoviruses coat protein family.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AB000709; BAA19169.1; -; mRNA.
 DR HSSP; P03570; 2TMV.
 DR SMR; P69509; 1-156.
 DR InterPro; IPR001337; TMV coat.
 DR Pfam; PF00721; TMV coat; 1.
 KW Acetylation; Capsid protein; Structural protein.
 FT INIT_MET 0 0 By similarity.
 FT MOD_RES 1 1 N-acetylalanine (By similarity).
 SQ SEQUENCE 156 AA; 17110 MW; B8D2E3E7C955BF73 CRC64;
 Query Match 58.1%; Score 43; DB 1; Length 156;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VENPMNRLVAETL 15
 Db 96 VENPQNPTTAETL 108
 RESULT 17
 COAT_PMMVS STANDARD; PRT; 156 AA.
 AC P69570; P29096;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Coat protein.
 GN Name=CP;
 OS Pepper mild mottle virus (strain Spain) (PMMV-S).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OC NCBI_TaxID=31745;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
 RX MEDLINE=92113528; PubMed=1765765;
 RA Alonso E., Garcia-Luque I., de la Cruz A., Wicke B.;
 RA Avila-Rincon M.J., Serra M.T., Castresana C., Diaz-Ruiz J.R.;
 RT "Nucleotide sequence of the genomic RNA of pepper mild mottle virus, a
 resistance-breaking tobamovirus in pepper.";
 RL J. Gen. Virol. 72:2875-2884(1991).
 CC -!- SIMILARITY: Belongs to the tobamoviruses coat protein family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; M81413; AAB02337.1; -; Genomic_RNA.
 DR FIR; JQ3315; VCTMPV.
 DR HSSP; P03570; 2TMV.
 DR SMR; P69510; 1-156.
 DR InterPro; IPR001337; TMV coat.
 DR Pfam; PF00721; TMV coat; 1.

KW Acetylation; Capsid protein; Structural protein.
 FT INIT_MET 0 0 By similarity.
 FT MOD_RES 1 1 N-acetylalanine (By similarity).
 SQ SEQUENCE 156 AA; 17110 MW; B8D2E3E7C955BF73 CRC64;
 Query Match 58.1%; Score 43; DB 1; Length 156;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VENPMNRLVAETL 15
 Db 96 VENPQNPTTAETL 108
 RESULT 18
 COAT_TOMKO STANDARD; PRT; 156 AA.
 ID COAT_TOMKO
 AC Q83482;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Coat protein.
 GN Name=CP;
 OS Tomato mosaic virus (strain Korean) (ToMV).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OC NCBI_TaxID=138313;
 OX [1]
 RN NUCLEOTIDE SEQUENCE [GENOMIC RNA].
 RA Park E.K., Lee C.H., Lee Y.G., Lee Y.H.;
 RT "Characterization of coat protein from TMV Korean tomato strain.";
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the tobamoviruses coat protein family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; J35074; AAA46589.1; -; Genomic_RNA.
 DR HSSP; P03570; 2TMV.
 DR SMR; Q83482; 1-156.
 DR InterPro; IPR001337; TMV coat.
 DR Pfam; PF00721; TMV coat; 1.
 KW Acetylation; Capsid protein; Structural protein.
 FT INIT_MET 0 0 By similarity.
 FT MOD_RES 1 1 N-acetylserine (By similarity).
 SQ SEQUENCE 156 AA; 17126 MW; B8CB04736FEAF41 CRC64;
 Query Match 58.1%; Score 43; DB 1; Length 156;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VENPMNRLVAETL 15
 Db 96 VENPQNPTTAETL 108
 RESULT 19
 Q6LER3_9VIRU PRELIMINARY; PRT; 157 AA.
 ID Q6LER3_9VIRU
 AC Q6LER3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Coat protein.
 OS Tobacco mosaic virus.
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OC NCBI_TaxID=12242;
 OX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=P;
 RA Nishimiya S.;

RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D13367; BAA02631.1; -; Genomic_RNA.
 DR SMR; Q6LER3; 2-157.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001337; TMV_coat.
 DR Pfam; PF00721; TMV_coat; 1.
 KW Capsid protein.
 SQ SEQUENCE 157 AA; 17241 MW; 7122837E9E86257 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
 |||||
 Db 97 VENPQNPTAETL 109

RESULT 20
 Q76M57 9VIRU PRELIMINARY; PRT; 157 AA.
 AC Q76M57
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Coat protein (Capsid protein).
 OS Pepper mild mottle virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OX NCBI_TaxID=12239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hamada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22255451; PubMed=12367724; DOI=10.1016/S0166-0934(02)00135-0;
 RA Letschert B., Adam G., Lesemann D.E., Willingmann P., Heinze C.;
 RA "Detection and differentiation of serologically cross-reacting
 RT tobamoviruses of economical importance by RT-PCR and RT-PCR-RFLP.";
 RL J. Virol. Methods 106:1-10(2002).
 DR EMBL; AB062053; BAB5800.1; -; Genomic RNA.
 DR EMBL; AJ429089; CAD22086.1; -; Genomic_RNA.
 DR SMR; Q76M57; 2-157.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001337; TMV_coat.
 DR Pfam; PF00721; TMV_coat; 1.
 KW Capsid protein.
 SQ SEQUENCE 157 AA; 17266 MW; 30056A6479EF1222 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
 |||||
 Db 97 VENPQNPTAETL 109

RESULT 21
 Q780A7 9VIRU PRELIMINARY; PRT; 157 AA.
 AC Q780A7
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE Coat protein.
 OS Pepper mild mottle virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OX NCBI_TaxID=12239;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Yoon J.Y., Choi J.K., Ryu K.H.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Takeuchi S., Hamada H., Kiba A., Hikichi Y., Okuno T.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Eiras M.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Huang Y.Y., Zhai X.L., Ma R.Q.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Kr;
 RA Yoon J., Choi J., Ryu K.;
 RT "Molecular characterization of pepper mild mottle virus Kr strain.";
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PMOV-CN;
 RA Liu F., Wang X., Zhou G.;
 RT "Nucleotide sequence analysis of the genome of the pepper mild mottle
 RT virus in China (PMOV).";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB084456; BAB91239.1; -; Genomic RNA.
 DR EMBL; AB119482; BAC85000.1; -; Genomic_RNA.
 DR EMBL; AF525080; AAM83090.1; -; mRNA.
 DR EMBL; AB126003; BAD90601.1; -; Genomic RNA.
 DR EMBL; AY859497; AAW55641.1; -; Genomic_RNA.
 DR EMBL; AY632863; AAT46356.1; -; Genomic_RNA.
 DR SMR; Q780A7; 2-157.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001337; TMV_coat.
 DR Pfam; PF00721; TMV_coat; 1.
 KW Capsid protein.
 SQ SEQUENCE 157 AA; 17241 MW; 7122837E9E86257 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
 |||||
 Db 97 VENPQNPTAETL 109

RESULT 22
 Q80P27 9VIRU PRELIMINARY; PRT; 157 AA.
 AC Q80P27;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Capsid protein.
 OS Pepper mild mottle virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
 OX NCBI_TaxID=12239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22255451; PubMed=12367724; DOI=10.1016/S0166-0934(02)00135-0;
 RA Letschert B., Adam G., Lesemann D.E., Willingmann P., Heinze C.;
 RA "Detection and differentiation of serologically cross-reacting
 RT tobamoviruses of economical importance by RT-PCR and RT-PCR-RFLP.";
 RL J. Virol. Methods 106:1-10(2002).
 DR EMBL; AJ429087; CAD22084.1; -; Genomic_RNA.
 DR HSSP; P03570; 2TMV.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.

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DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
SQ SEQUENCE 157 AA; 17310 MW; 47703D64B776081A CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
DB 97 VENPQNPTTAETL 109

RESULT 23
Q91E32_9VIRU
ID Q91E32_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91E32;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RC STRAIN=Ta;
RX MEDLINE=22255465; PubMed=12367738; DOI=10.1016/S0166-0934(02)00144-1;
RA Velasco L., Janssen D., Ruiz-Garcia L., Segundo E., Cuadrado I.M.;
RT "The complete nucleotide sequence and development of a differential
RT detection assay for a pepper mild mottle virus (PMoV) isolate that
RT overcomes L3 resistance in pepper."
RL J. Virol. Methods 106:135-140(2002).
DR EMBL; AJ308226; CAC59958.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91E32; 2-157.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.
SQ SEQUENCE 157 AA; 17252 MW; D2C9E9DC426CB9AA CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
DB 97 VENPQNPTTAETL 109

RESULT 24
Q91U97_9VIRU
ID Q91U97_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91U97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Coat protein (Capsid protein).
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Hamada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255451; PubMed=12367724; DOI=10.1016/S0166-0934(02)00135-0;
RA Letschert B., Adam G., Lesemann D.E., Willingmann P., Heinze C.;
RT "Detection and differentiation of serologically cross-reacting
RT tobamoviruses of economical importance by RT-PCR and RT-PCR-RELP."
J. Virol. Methods 106:1-10(2002).
DR EMBL; AB062054; BAB5801.1; -; Genomic_RNA.
DR EMBL; AJ429088; CAD22085.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91U97; 2-157.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.
SQ SEQUENCE 157 AA; 17241 MW; 7472D5980A5ED257 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
DB 97 VENPQNPTTAETL 109

RESULT 25
Q91U98_9VIRU
ID Q91U98_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91U98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Hamada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062052; BAB55799.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91U98; 2-157.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.
SQ SEQUENCE 157 AA; 17255 MW; BBAP2818317760CA CRC64;

Query Match 58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
DB 97 VENPQNPTTAETL 109

RESULT 26
Q91U99_9VIRU
ID Q91U99_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91U99;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Hamada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062051; BAB55798.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91U99; 2-157.

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```
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.
SQ SEQUENCE 157 AA; 17236 MW; E90E1098121AGBBB CRC64;

Query Match      58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
Db 97 VENPQNPTTAETL 109

RESULT 27
Q91UA0_9VIRU
ID Q91UA0_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91UA0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hanada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062050; BAB55797.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91UA0; 2-157.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.
SQ SEQUENCE 157 AA; 17226 MW; A93C0CFB2F493B6B CRC64;

Query Match      58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
Db 97 VENPQNPTTAETL 109

RESULT 28
Q91UA1_9VIRU
ID Q91UA1_9VIRU PRELIMINARY; PRT; 157 AA.
AC Q91UA1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Pepper mild mottle virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hanada H., Takeuchi S., Kiba A., Hikichi Y., Okuno T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062049; BAB55796.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q91UA1; 2-157.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Capsid protein.

SQ SEQUENCE 157 AA; 17210 MW; A80EOCE80E761BA7 CRC64;

Query Match      58.1%; Score 43; DB 2; Length 157;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
Db 97 VENPQNPTTAETL 109

RESULT 29
COAT_PMVV0
ID COAT_PMVV0 STANDARD; PRT; 158 AA.
AC Q9WDG3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Coat protein.
GN Name=CP;
OS Pepper mild mottle virus (strain P0) (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=138303;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Sohn S.-H., Hahn J.-H., Hwang Y.-S.;
RT "The coat protein gene of Pepper Mild Mottle Virus isolated from Hot
   pepper in Korea.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the tobamoviruses coat protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use as long as its content is in no way modified and this statement is not
   removed.
CC EMBL; AF103776; AAD20287.1; -; mRNA.
DR HSSP; P03570; 2TMV.
DR SMR; Q9WDG3; 1-158.
DR InterPro; IPR001337; TMV_coat.
DR Pfam; PF00721; TMV_coat; 1.
KW Acetylation; Capsid protein; Structural protein.
FT INETMET 0 By similarity.
FT MOD_RES 1 1 N-acetylalanine (By similarity).
SQ SEQUENCE 158 AA; 17451 MW; A31C592C0A01D79A CRC64;

Query Match      58.1%; Score 43; DB 1; Length 159;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VENPMNRLVAETL 15
Db 96 VENPQNPTTAETL 108

RESULT 30
Q83483_9VIRU
ID Q83483_9VIRU PRELIMINARY; PRT; 158 AA.
AC Q83483;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coat protein.
OS Tobacco mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12242;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Park E.K., Lee C.H., Lee Y.G., Lee Y.H.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L35073; AAA46588.1; -; Genomic_RNA.
DR HSSP; P03570; 2TMV.
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DR SMR; Q83483; 2-148.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; P:structural molecule activity; IEA.
 DR InterPro; IPR001337; TMV_coat.
 DR Pfam; PF00721; TMV_coat; 1.
 KW Capsid protein.
 SQ SEQUENCE 158 AA; 17456 MW; 8F4A2E610E5F41A5 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 158;
 Best Local Similarity 69.2%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 VENPMNRLVAETL 15
 |||||
 Db 97 VENPQNPTTAETL 109

Search completed: December 17, 2005, 07:32:57
 Job time : 233 secs

77	44	59.5	236934	9	AC084073	AC084073 Mus muscu	150	42	56.8	27024	15	AC139172	AC139172 Oryza sat
78	44	59.5	253649	14	AC106142	AC106142 Rattus no	151	42	56.8	34794	2	UI3071	UI3071 Caenorhabdi
79	44	59.5	280257	14	AC096983	AC096983 Rattus no	152	42	56.8	34836	8	AC006522	AC006522 Homo sapi
80	43.5	58.8	110000	1	CP000058.38	Continuation (39 o	153	42	56.8	38675	8	AC015552	AC015552 Homo sapi
81	43	58.1	210	6	AR553628_49	AR553628 Sequence	154	42	56.8	42441	14	AC109339	AC109339 Homo sapi
82	43	58.1	474	13	AB062049	AB062049 Pepper mi	155	42	56.8	42441	14	AC109339	AC109339 Homo sapi
83	43	58.1	474	13	AB062050	AB062050 Pepper mi	156	42	56.8	42441	14	AC109339	AC109339 Homo sapi
84	43	58.1	474	13	AB062051	AB062051 Pepper mi	157	42	56.8	42441	14	AC109339	AC109339 Homo sapi
85	43	58.1	474	13	AB062052	AB062052 Pepper mi	158	42	56.8	42441	14	AC109339	AC109339 Homo sapi
86	43	58.1	474	13	AB062053	AB062053 Pepper mi	159	42	56.8	42441	14	AC109339	AC109339 Homo sapi
87	43	58.1	474	13	AB062054	AB062054 Pepper mi	160	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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93	43	58.1	474	13	AB119482	AB119482 Pepper mi	166	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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97	43	58.1	474	13	AB119482	AB119482 Pepper mi	170	42	56.8	42441	14	AC109339	AC109339 Homo sapi
98	43	58.1	474	13	AB119482	AB119482 Pepper mi	171	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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118	43	58.1	474	13	AB119482	AB119482 Pepper mi	191	42	56.8	42441	14	AC109339	AC109339 Homo sapi
119	43	58.1	474	13	AB119482	AB119482 Pepper mi	192	42	56.8	42441	14	AC109339	AC109339 Homo sapi
120	43	58.1	474	13	AB119482	AB119482 Pepper mi	193	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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127	43	58.1	474	13	AB119482	AB119482 Pepper mi	200	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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131	43	58.1	474	13	AB119482	AB119482 Pepper mi	204	42	56.8	42441	14	AC109339	AC109339 Homo sapi
132	43	58.1	474	13	AB119482	AB119482 Pepper mi	205	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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136	43	58.1	474	13	AB119482	AB119482 Pepper mi	209	42	56.8	42441	14	AC109339	AC109339 Homo sapi
137	43	58.1	474	13	AB119482	AB119482 Pepper mi	210	42	56.8	42441	14	AC109339	AC109339 Homo sapi
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143	42	56.8	363	6	AX072434	AX072434 Sequence	216	42	56.8	21584	14	AC128591	AC128591 Rattus no
144	42	56.8	443	10	AX026135	AX026135 Rattus no	217	42	56.8	21571	14	AC137358	AC137358 Rattus no
145	42	56.8	601	10	BV295269	BV295269 S232P65FP	218	42	56.8	21571	14	AC137358	AC137358 Rattus no
146	42	56.8	655	10	BV274785	BV274785 S232P6304	219	42	56.8	22204	14	AC162215	AC162215 Bos tauru
147	42	56.8	1189	8	HSAPWR2	HSAPWR2 Homo sapi	220	42	56.8	22204	14	AC130906	AC130906 Rattus no
148	42	56.8	2142	2	AF121264	AF121264 Onchocerc	221	42	56.8	22469	14	AC137364	AC137364 Rattus no
149	42	56.8	14707	6	AR308080	AR308080 Sequence	222	42	56.8	227437	14	AC119698	AC119698 Rattus no

223	c	223	56.8	22785	9	AC149087	AC149087 Mus muscu	c	296	41	55.4	110000	1	AJ745949_03	Continuation (4 of
224	c	224	56.8	231179	14	AC096129	AC096129 Rattus no	c	297	41	55.4	110000	14	AP006494_5	Continuation (6 of
225	c	225	56.8	231383	5	AL844512	AL844512 Zebrafish	c	298	41	55.4	110000	14	AP006501_03	Continuation (4 of
226	c	226	56.8	254753	14	AC153713	AC153713 Bos tauru	c	299	41	55.4	110000	15	AP008214_228	Continuation (229
227	c	227	56.8	269948	2	AE003559	AE003559 Drosophil	c	300	41	55.4	110000	15	AP008216_026	Continuation (27 o
228	c	228	56.8	270850	14	AC095807	AC095807 Rattus no	c	301	41	55.4	110000	15	AP008217_050	Continuation (51 o
229	c	229	56.8	294330	14	AC130768	AC130768 Rattus no	c	302	41	55.4	110000	15	CR382124_12	Continuation (13 o
230	c	230	56.8	301934	15	AE017110	AE017110 Oryza sat	c	303	41	55.4	110000	15	AP008207_152	Continuation (153
231	c	231	56.8	305518	14	AC006879	AC006879 Caenorhab	c	304	41	55.4	110000	15	AP008209_034	Continuation (35 o
232	c	232	56.8	339972	15	OSA307662	AJ307662 Oryza sat	c	305	41	55.4	110000	15	AP008209_035	Continuation (36 o
233	c	233	56.8	346296	15	AF090447	AF090447 Zea mays	c	306	41	55.4	110000	15	AP008210_261	Continuation (262
234	c	234	55.4	238	6	BD189779	BD189779 Polynucle	c	307	41	55.4	110000	15	AP008211_284	Continuation (285
235	c	235	55.4	242	13	AF336007	AF336007 Swine hep	c	308	41	55.4	111876	15	ATF4110	AL035525 Arabidops
236	c	236	55.4	255	6	BD189777	BD189777 Polynucle	c	309	41	55.4	112886	5	CR759914	CR759914 Zebrafish
237	c	237	55.4	326	13	AB189927	AB189927 Hepatitis	c	310	41	55.4	113201	8	AC117509	AC117509 Homo sapi
238	c	238	55.4	516	15	AF417299	AF417299 Caenanea	c	311	41	55.4	117439	15	AC122163	AC122163 Medicago
239	c	239	55.4	543	11	AV774365	AV774365 Synthetic	c	312	41	55.4	117439	15	OSJN00211	AL663010 Oryza sat
240	c	240	55.4	623	5	CR390403	CR390403 Gallus ga	c	313	41	55.4	119500	15	AC098832	AC098832 Oryza sat
241	c	241	55.4	643	10	G56830	G56830 SHGC-102369	c	314	41	55.4	121970	14	AC166703	AC166703 Bos tauru
242	c	242	55.4	654	8	AF339060	AF339060 Salmir b	c	315	41	55.4	123570	8	AC022846	AC022846 Homo sapi
243	c	243	55.4	719	10	BV633686	BV633686 S21P6149	c	316	41	55.4	125381	4	AY644517	AY644517 Bos tauru
244	c	244	55.4	941	6	CQ614715	CQ614715 Sequence	c	317	41	55.4	127500	8	AP006564	AP006564 Homo sapi
245	c	245	55.4	942	10	AB093400	AB093400 Bos tauru	c	318	41	55.4	135301	15	AP003198	AP003198 Oryza sat
246	c	246	55.4	1150	2	AV118443	AV118443 Drosophil	c	319	41	55.4	136477	14	AC157873	AC157873 Loxodonta
247	c	247	55.4	1798	6	AX509604	AX509604 Sequence	c	320	41	55.4	137127	15	AC145323	AC145323 Oryza sat
248	c	248	55.4	1834	8	AF374234	AF374234 Ateles ge	c	321	41	55.4	139685	14	AC153082	AC153082 Ornithorh
249	c	249	55.4	1881	8	CJA297563	AJ797563 Callithri	c	322	41	55.4	150436	14	AC157879	AC157879 Loxodonta
250	c	250	55.4	2000	6	AX595654	AX595654 Sequence	c	323	41	55.4	150620	14	AC107225	AC107225 Oryza sat
251	c	251	55.4	2000	6	AX819836	AX819836 Sequence	c	324	41	55.4	152703	14	CR925857	CR925857 Danio rer
252	c	252	55.4	2000	6	AX830866	AX830866 Sequence	c	325	41	55.4	153957	14	AC156102	AC156102 Bos tauru
253	c	253	55.4	2442	6	BD189772	BD189772 Polynucle	c	326	41	55.4	155828	9	AC132618	AC132618 Mus muscu
254	c	254	55.4	2941	6	CQ614714	CQ614714 Sequence	c	327	41	55.4	156174	9	AL645687	AL645687 Mouse DNA
255	c	255	55.4	4074	15	SCYNL132W	D71408 S.cerevisia	c	328	41	55.4	157035	14	AC131642	AC131642 Rattus no
256	c	256	55.4	4354	15	ATHAYPEA	D61393 Arabidopsis	c	329	41	55.4	157095	14	AC160771	AC160771 Bos tauru
257	c	257	55.4	5138	6	BD189766	BD189766 Polynucle	c	330	41	55.4	160517	14	AC156732	AC156732 Bos tauru
258	c	258	55.4	5411	1	AB010124	AB010124 Staphyloc	c	331	41	55.4	161361	14	AC150921	AC150921 Bos tauru
259	c	259	55.4	6496	6	CQ614777	CQ614777 Sequence	c	332	41	55.4	162037	9	AC137516	AC137516 Mus muscu
260	c	260	55.4	7230	6	BD189810	BD189810 Polynucle	c	333	41	55.4	162075	8	AC152070	AC152070 Pan trogl
261	c	261	55.4	7230	13	AP003430	AP003430 Hepatitis	c	334	41	55.4	163297	14	AC157623	AC157623 Bos tauru
262	c	262	55.4	7233	6	BD189807	BD189807 Polynucle	c	335	41	55.4	163862	14	AC092911	AC092911 Homo sapi
263	c	263	55.4	7240	13	AB074920	AB074920 Hepatitis	c	336	41	55.4	164339	14	AC131894	AC131894 Gallus ga
264	c	264	55.4	9459	1	AE011340	AE011340 Leptospir	c	337	41	55.4	164548	8	AC079613	AC079613 Homo sapi
265	c	265	55.4	9942	9	AF329470	AF329470 Rattus no	c	338	41	55.4	165082	14	AC026559	AC026559 Homo sapi
266	c	266	55.4	10708	9	RNITPR2R	AF16777 Rat ITPR2 g	c	339	41	55.4	165475	9	AC159295	AC159295 Mus muscu
267	c	267	55.4	14376	1	AE005688	AE005688 Caulobact	c	340	41	55.4	166266	9	AC154835	AC154835 Mus muscu
268	c	268	55.4	21915	1	AE008824	AE008824 Salmoneil	c	341	41	55.4	167587	15	AP002914	AP002914 Oryza sat
269	c	269	55.4	2469	14	AC019983	AC019983 Drosophil	c	342	41	55.4	168141	9	AC146598	AC146598 Mus muscu
270	c	270	55.4	30589	2	CRZK666	Z49132 Caenorhabdi	c	343	41	55.4	169588	15	AP006461	AP006461 Oryza sat
271	c	271	55.4	3245	15	AP006845	AP006845 Oryza sat	c	344	41	55.4	169755	14	AC163479	AC163479 Bos tauru
272	c	272	55.4	36137	8	AC005933	AC005933 Homo sapi	c	345	41	55.4	170737	9	AC129180	AC129180 Mus muscu
273	c	273	55.4	39170	8	AC067969	AC067969 Homo sapi	c	346	41	55.4	170804	14	AC156463	AC156463 Bos tauru
274	c	274	55.4	41181	15	SPAC23G3	AL138854 S.pombe c	c	347	41	55.4	171454	2	AC007137	AC007137 Drosophil
275	c	275	55.4	41812	2	CB00334	Z66519 Caenorhabdi	c	348	41	55.4	172087	14	AC163843	AC163843 Bos tauru
276	c	276	55.4	43481	15	SCCHIV43	Z46843 S.cerevisia	c	349	41	55.4	173804	8	HS1030M6	AL035089 Human DNA
277	c	277	55.4	47850	8	AL358237	AL358237 Human DNA	c	350	41	55.4	175499	14	AL645737	AL645737 Homo sapi
278	c	278	55.4	61095	14	AC119430	AC119430 Mus muscu	c	351	41	55.4	175590	14	AF307159	AF307159 Homo sapi
279	c	279	55.4	66502	14	AC164965	AC164965 Bos tauru	c	352	41	55.4	178026	9	AC102922	AC102922 Mus muscu
280	c	280	55.4	69470	5	CR385069	CR385069 Zebrafish	c	353	41	55.4	178122	14	AC095848	AC095848 Rattus no
281	c	281	55.4	78552	14	AC021253	AC021253 Homo sapi	c	354	41	55.4	180327	14	AC113792	AC113792 Rattus no
282	c	282	55.4	78847	14	AC166695	AC166695 Bos tauru	c	355	41	55.4	181761	14	AC090199	AC090199 Homo sapi
283	c	283	55.4	80664	14	AC162548	AC162548 Bos tauru	c	356	41	55.4	181941	8	AC022910	AC022910 Homo sapi
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285	c	285	55.4	81775	14	AC166041	AC166041 Bos tauru	c	358	41	55.4	182160	14	AC142550	AC142550 Danio rer
286	c	286	55.4	83188	14	AC166672	AC166672 Bos tauru	c	359	41	55.4	183555	9	AC124582	AC124582 Mus muscu
287	c	287	55.4	87080	15	AC004747	AC004747 Arabidops	c	360	41	55.4	184079	14	AC161998	AC161998 Bos tauru
288	c	288	55.4	94482	15	ATF26P21	AL031804 Arabidops	c	361	41	55.4	184806	14	AC155871	AC155871 Bos tauru
289	c	289	55.4	96707	14	AC165010	AC165010 Bos tauru	c	362	41	55.4	185367	14	AC164189	AC164189 Oryza sat
290	c	290	55.4	97110	8	AL591521	AL591521 Human DNA	c	363	41	55.4	185904	15	AC079852	AC079852 Oryza sat
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294	c	294	55.4	106763	5	BX294388	BX294388 Zebrafish	c	367	41	55.4	190662	14	AC160034	AC160034 Bos tauru
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C 372	41	55.4	194006	8	AC074044	AC074044 Homo sapi	C 445	41	55.4	273962	14	AC160157	AC160157 Bos tauru
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C 376	41	55.4	197063	14	AC159724	AC159724 Bos tauru	C 449	41	55.4	283651	14	AC153396	AC153396 Bos tauru
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C 379	41	55.4	198916	14	AC145008	AC145008 Bos tauru	C 452	41	55.4	291738	14	AC097744	AC097744 Rattus no
C 380	41	55.4	199111	14	AC158083	AC158083 Bos tauru	C 453	41	55.4	296706	14	CR759751	CR759751 Danio rer
C 381	41	55.4	202103	14	AC121195	AC121195 Rattus no	C 454	41	55.4	297936	14	AC156666	AC156666 Bos tauru
C 382	41	55.4	202353	14	AC164064	AC164064 Bos tauru	C 455	41	55.4	298590	14	AC159087	AC159087 Bos tauru
C 383	41	55.4	203759	14	AC152761	AC152761 Bos tauru	C 456	41	55.4	298896	14	AC151081	AC151081 Bos tauru
C 384	41	55.4	204091	14	AC152442	AC152442 Bos tauru	C 457	41	55.4	300029	15	AE017055	AE017055 Oryza sat
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C 386	41	55.4	205028	9	AC154862	AC154862 Mus muscu	C 459	41	55.4	314531	14	CR388228	CR388228 Danio rer
C 387	41	55.4	205114	14	AC162489	AC162489 Bos tauru	C 460	41	55.4	315743	14	AC162474	AC162474 Bos tauru
C 388	41	55.4	205371	14	AC157157	AC157157 Bos tauru	C 461	41	55.4	316511	14	AC159369	AC159369 Bos tauru
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C 390	41	55.4	208846	14	AC162339	AC162339 Bos tauru	C 463	41	55.4	345542	14	AC120727	AC120727 Rattus no
C 391	41	55.4	213195	14	AC156422	AC156422 Bos tauru	C 464	41	55.4	349652	1	BX571866	BX571866 Photorhab
C 392	41	55.4	213380	14	AC156507	AC156507 Bos tauru	C 465	41	55.4	349980	6	AX770906	AX770906 Sequence
C 393	41	55.4	214259	14	AC160786	AC160786 Bos tauru	C 466	40.5	54.7	1262	1	AF274326	AF274326 Pseudomon
C 394	41	55.4	215374	14	AC150765	AC150765 Bos tauru	C 467	40.5	54.7	78855	14	AC166084	AC166084 Bos tauru
C 395	41	55.4	216226	14	AC137215	AC137215 Rattus no	C 468	40.5	54.7	80169	14	AC164773	AC164773 Bos tauru
C 396	41	55.4	219466	14	AC164018	AC164018 Bos tauru	C 469	40	54.1	165	6	CQ751328	CQ751328 Sequence
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C 398	41	55.4	220714	14	CT010454	CT010454 Mus muscu	C 471	40	54.1	326	13	AB200243	AB200243 Hepatitis
C 399	41	55.4	221566	14	AC161951	AC161951 Bos tauru	C 472	40	54.1	430	2	AF300460	AF300460 Axinella
C 400	41	55.4	222859	14	AC159051	AC159051 Bos tauru	C 473	40	54.1	459	6	CQ173785	CQ173785 Sequence
C 401	41	55.4	225884	14	AC098500	AC098500 Rattus no	C 474	40	54.1	524	10	BV002022	BV002022 S209P6145
C 402	41	55.4	227026	9	AC113476	AC113476 Mus muscu	C 475	40	54.1	567	6	CQ178166	CQ178166 Sequence
C 403	41	55.4	227119	14	BX119971	BX119971 Danio rer	C 476	40	54.1	628	10	BV328837	BV328837 S241P6199
C 404	41	55.4	227199	14	AC094896	AC094896 Rattus no	C 477	40	54.1	672	10	BV517386	BV517386 r1t18b10.
C 405	41	55.4	227378	14	AC149654	AC149654 Bos tauru	C 478	40	54.1	708	10	BV538201	BV538201 G591P6358
C 406	41	55.4	228030	14	AC164232	AC164232 Bos tauru	C 479	40	54.1	718	8	HUMDTN21	HUMDTN21 Human dystr
C 407	41	55.4	228079	14	AC156851	AC156851 Bos tauru	C 480	40	54.1	725	10	BV541075	BV541075 G591P5139
C 408	41	55.4	228307	14	AC153699	AC153699 Bos tauru	C 481	40	54.1	743	10	BV646733	BV646733 S217P6032
C 409	41	55.4	228864	14	AC155755	AC155755 Bos tauru	C 482	40	54.1	769	8	BSA344097	BSA344097 Homo sapi
C 410	41	55.4	229327	14	AC160441	AC160441 Bos tauru	C 483	40	54.1	795	10	BV542081	BV542081 Mycoplasma
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C 412	41	55.4	231452	14	AC160482	AC160482 Bos tauru	C 485	40	54.1	928	10	BV520708	BV520708 Mycoplasma
C 413	41	55.4	232542	14	AC159393	AC159393 Bos tauru	C 486	40	54.1	955	1	AF314228	AF314228 Mycoplasma
C 414	41	55.4	232726	14	AC159787	AC159787 Bos tauru	C 487	40	54.1	1055	1	AF143444	AF143444 Sinorhizo
C 415	41	55.4	232737	2	AE003660	AE003660 Drosophila	C 488	40	54.1	1125	6	CQ733313	CQ733313 Sequence
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C 417	41	55.4	234856	14	AC157006	AC157006 Bos tauru	C 490	40	54.1	1468	15	YLSRPP19A	YLSRPP19A
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C 419	41	55.4	237065	14	AC128999	AC128999 Rattus no	C 492	40	54.1	2080	5	BC090464	BC090464 Danio rer
C 420	41	55.4	237450	14	AC095092	AC095092 Rattus no	C 493	40	54.1	2194	1	SME242574	SME242574 Sinorhizo
C 421	41	55.4	237986	14	AC106932	AC106932 Rattus no	C 494	40	54.1	2216	1	AF488710	AF488710 Mycoplasma
C 422	41	55.4	238712	14	AC115308	AC115308 Rattus no	C 495	40	54.1	2310	6	CQ817586	CQ817586 Sequence
C 423	41	55.4	239760	14	AC095113	AC095113 Rattus no	C 496	40	54.1	2518	8	HSU46744	HSU46744 Human dystr
C 424	41	55.4	239905	14	AC154363	AC154363 Bos tauru	C 497	40	54.1	2591	6	AX833370	AX833370 Sequence
C 425	41	55.4	243486	14	AC153622	AC153622 Bos tauru	C 498	40	54.1	2591	8	AK095037	AK095037 Homo sapi
C 426	41	55.4	244183	14	AC160787	AC160787 Bos tauru	C 499	40	54.1	2695	4	AF415201S1	AF415201 Sus scrofa
C 427	41	55.4	244429	14	AC155061	AC155061 Bos tauru	C 500	40	54.1	3272	15	AY255705	AY255705 Mangifera
C 428	41	55.4	248040	14	AC163839	AC163839 Bos tauru							
C 429	41	55.4	248151	14	AC157338	AC157338 Bos tauru							
C 430	41	55.4	249153	14	AC162990	AC162990 Bos tauru							
C 431	41	55.4	250898	14	AC153042	AC153042 Bos tauru							
C 432	41	55.4	252650	14	AC160208	AC160208 Bos tauru							
C 433	41	55.4	255140	14	AC160814	AC160814 Bos tauru							
C 434	41	55.4	256265	14	AC122943	AC122943 Rattus no							
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C 438	41	55.4	258031	14	AC163117	AC163117 Bos tauru							
C 439	41	55.4	261408	14	BX950188	BX950188 Danio rer							
C 440	41	55.4	266711	14	AC163472	AC163472 Bos tauru							
C 441	41	55.4	269573	14	AC162560	AC162560 Bos tauru							

ALIGNMENTS

RESULT 1	BD211562	345 bp	DNA	linear	PAT 17-JUL-2003
BD211562	Canine and feline immunoregulatory proteins, nucleic acid molecules				
LOCUS	BD211562.1	GI:33021332			
DEFINITION	Canine and feline immunoregulatory proteins, nucleic acid molecules				
ACCESSION	BD211562				
VERSION	BD211562.1				
KEYWORDS	JP 2002516104-A/68.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 345)
 AUTHORS Sim,G., Yang S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
 JOURNAL Patent: JP 2002516104-A 68 04-JUN-2002;

HESSA CORP

COMMENT OS Canis familiaris (dog)
 PN JP 2002516104-A/68
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000551002
 PR 29-MAY-1998 US 60/087306

PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
 C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
 PC A61K39/395,
 PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
 PC C07K14/54,
 PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
 G01N33/15,
 PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
 and feline immunoregulatory proteins, nucleic acid CC
 molecules and
 CC method of using the same
 FH Key Location/Qualifiers
 FT CDS (1)..(345).

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 /mol_type="genomic DNA"
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 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-10-787-382-20 (1-15) x BD211562 (1-345)
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RESULT 2
 BD211563/c
 LOCUS BD211563 345 bp DNA linear PAT 17-JUL-2003
 DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
 ACCESSION BD211563
 VERSION BD211563.1 GI:33021333
 KEYWORDS JP 2002516104-A/69.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 345)
 AUTHORS Sim,G., Yang S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
 JOURNAL Patent: JP 2002516104-A 69 04-JUN-2002;

HESSA CORP

COMMENT OS Canis familiaris (dog)
 PN JP 2002516104-A/69
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000551002
 PR 29-MAY-1998 US 60/087306

PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC

C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
 PC A61K39/395,
 PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
 PC C07K14/54,
 PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
 G01N33/15,
 PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
 and feline immunoregulatory proteins, nucleic acid CC
 molecules and
 CC method of using the same
 FH Key Location/Qualifiers
 FT source 1..345
 /organism="Canis familiaris (dog)".

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ORIGIN
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 Pred. No.: 3.57e-06 Length: 345
 Score: 74.00 Matches: 15
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RESULT 3
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 LOCUS AR241540 345 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 85 from patent US 6471957.
 ACCESSION AR241540
 VERSION AR241540.1 GI:27287249
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof
 JOURNAL Patent: US 6471957-A 85 29-OCT-2002;
 EPX; Heska Corporation; Fort Collins, CO;

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ORIGIN
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 Pred. No.: 3.57e-06 Length: 345
 Score: 74.00 Matches: 15
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RESULT 4
 AR241541/c
 LOCUS AR241541 345 bp DNA linear PAT 20-DEC-2002

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DEFINITION Sequence 87 from patent US 6471957.
ACCESSION AR241541
VERSION AR241541.1 GI:27287250
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 87 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
EPX;
FEATURES
source
Location/Qualifiers
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Alignment Scores:
Pred. No.: 345 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 345 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 301
RESULT 5
AR254496
LOCUS AR254496 345 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 85 from patent US 6482403.
ACCESSION AR254496
VERSION AR254496.1 GI:27303384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 85 19-NOV-2002;
Heska Corporation; Fort Collins, CO
FEATURES
source
Location/Qualifiers
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Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 1 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 45
RESULT 6
AR254497/c
LOCUS AR254497 345 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 87 from patent US 6482403.
ACCESSION AR254497
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VERSION AR254497.1 GI:27303385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 87 19-NOV-2002;
Heska Corporation; Fort Collins, CO
FEATURES
source
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 345 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-787-382-20 (1-15) x AR254497 (1-345)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
DB 345 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 301
RESULT 7
AR091133
LOCUS AF091133 356 bp mRNA linear MAM 04-AUG-1999
DEFINITION Canis familiaris interleukin-5 mRNA, partial cds.
ACCESSION AF091133
VERSION AF091133.1 GI:5690203
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 356)
AUTHORS German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
TITLE Cloning and sequencing of canine interleukin-5
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 356)
AUTHORS German,A.J., Helps,C.R., Harley,R., Hall,E.J. and Day,M.J.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1998) Department of Clinical Veterinary Science,
University of Bristol, Langford House, Langford, Bristol, North
Somerset BS40 5DU, United Kingdom
FEATURES
source
Location/Qualifiers
1..356
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/db_xref="taxon:9615"
<!.>356
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/product="interleukin-5"
/protein_id="AAD46991.1"
/db_xref="GI:5690204"
/translation="LGVLCSAFAVENPMNLVAETITLLSTHRTWLTIGDNLWIPPE
NNHQICIKVEFGIDITLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGKKKVTN
FLNYLQLFLGVNNTW"
ORIGIN
Alignment Scores:
Pred. No.: 345 Length: 356
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 4.26e-06 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR241538 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
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 Db 58 TTTCGTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 102

RESULT 11

AR241539/c AR241539 402 bp DNA linear PAT 20-DEC-2002

LOCUS Sequence 84 from patent US 6471957.

DEFINITION AR241539

ACCESSION AR241539

VERSION AR241539.1 GI:27287248

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 402)

AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine IL-4 immunoregulatory proteins and uses thereof

JOURNAL Patent: US 6471957-A 84 29-OCT-2002;

Heska Corporation; Fort Collins, CO;

EPX;

FEATURES

source

1..402

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 4.26e-06 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR241539 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 |||||
 Db 345 TTTCGTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 301

RESULT 12

AR254494 AR254494 402 bp DNA linear PAT 20-DEC-2002

LOCUS Sequence 83 from patent US 6482403.

DEFINITION AR254494

ACCESSION AR254494

VERSION AR254494.1 GI:27303382

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 402)

AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine IL-13 immunoregulatory proteins and uses thereof

JOURNAL Patent: US 6482403-A 83 19-NOV-2002;

Heska Corporation; Fort Collins, CO

FEATURES

source

1..402

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 4.26e-06 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR254494 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 |||||
 Db 58 TTTCGTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 102

RESULT 13

AR254495/c

LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 84 from patent US 6482403.

ACCESSION AR254495

VERSION AR254495.1 GI:27303383

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 402)

AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine IL-13 immunoregulatory proteins and uses thereof

JOURNAL Patent: US 6482403-A 84 19-NOV-2002;

Heska Corporation; Fort Collins, CO

FEATURES

source

1..402

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 4.26e-06 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR254495 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 |||||
 Db 345 TTTCGTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 301

RESULT 14

AR300436

LOCUS AR300436 405 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 1 from patent US 6537781.

ACCESSION AR300436

VERSION AR300436.1 GI:31687875

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 405)

AUTHORS Guo,H., Lawton,R., Mermer,B. and Aliyappa,A.P.

TITLE Methods and compositions concerning canine interleukin 5

JOURNAL Patent: US 6537781-A 1 25-MAR-2003;

IDEXX Laboratories, Inc.; Westbrook, ME

FEATURES

source

1..405

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores: 4.3e-06 Length: 405

Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR300436 (1-405)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
58 TTTCGTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 102

RESULT 15
LOCUS AX083939
DEFINITION Sequence 1 from Patent WO0111049.
ACCESSION AX083939
VERSION AX083939.2 GI:14532940
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1
AUTHORS Guo, H., Lawton, R., Mermer, B. and Aiyappa, A.P.
TITLE Methods and compositions concerning canine interleukin 5
JOURNAL IDEX LABORATORIES, INC. (US)
COMMENT On Jun 24, 2001 this sequence version replaced gi:13185501.

FEATURES
source 1..405
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"

ORIGIN
Alignment Scores:
Pred. No.: 4.3e-06 Length: 405
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AX083939 (1-405)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
58 TTTCGTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 102

RESULT 16
AF331919
LOCUS AF331919
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION AF331919
VERSION AF331919.1 GI:15919180
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 610)
AUTHORS Yang, S., Sellina, K.S., Weber, E. and McCall, C.
TITLE Canine interleukin-5: molecular characterization of the gene and expression of biologically active recombinant protein
JOURNAL J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
PUBMED 11440633
REFERENCE 2 (bases 1 to 610)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613

Prospect Parkway, Ft Collins, CO 80525, USA
Location/Qualifiers
1..610
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
1..28
29..433
/note="IL-5"
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/product="interleukin-5"
/protein_id="AAL10715.1"
/db_xref="GI:15919181"
/translation="MRMLNLNLSLALGAAYVSFAVENPMRNLVAETLTLLSTHRTWL
IGDNLMIPTPENKHQCIEVFQGDITLKNQTAHGEAVDKLFQNLSLIKHIERQK
KRCAGERWRVTKFLDYLVQLVGLVINTWTPS"
433..610

5'UTR
CDS
3'UTR
ORIGIN

Alignment Scores:
Pred. No.: 6.91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x AF331919 (1-610)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
86 TTTCGTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 130

Db
RESULT 17
LOCUS BD211558
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION BD211558
VERSION BD211558.1 GI:33021328
KEYWORDS JP 2002516104-A/64
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 610)
AUTHORS Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL Patent: JP 2002516104-A 64 04-JUN-2002;
HESKA CORP
COMMENT OS Canis familiaris (dog)
PN JP 2002516104-A/64
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395,
PC A61K39/395,
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
FT CDS (29)..(430).
1..610
/organism="Canis familiaris"

/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN

Alignment Scores:
Pred. No.: 6.91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x BD211558 (1-610)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
DB 86 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 130

RESULT 18

BD211559/c
LOCUS
DEFINITION
Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same. PAT 17-JUL-2003
ACCESSION
BD211559
VERSION
BD211559.1 GI:33021329
KEYWORDS
JP 2002516104-A/65.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 610)
AUTHORS
Sim,G., Yang,S., Dreibitz,M.J. and Wonderling,R.S.
TITLE
Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL
Patent: JP 2002516104-A 65 04-JUN-2002;
COMMENT
OS Canis familiaris (dog)
PN JP 2002516104-A/65
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,
PC A61K39/395,
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
PH Key Location/Qualifiers
FT source 1..610
FT /organism="Canis familiaris (dog)"

FEATURES

source
1..610
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN

Alignment Scores:
Pred. No.: 6.91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x BD211559 (1-610)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
DB 525 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 481

RESULT 19

AR241537/c
LOCUS
DEFINITION
Sequence 80 from patent US 6471957. PAT 20-DEC-2002
ACCESSION
AR241537
VERSION
AR241537.1 GI:27287245
KEYWORDS
US 6471957-A 80 29-OCT-2002;
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 610)
AUTHORS
Sim,G.-K., Yang,S., Dreibitz,M.J. and Wonderling,R.S.
TITLE
Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL
Patent: US 6471957-A 80 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
EPX;

FEATURES

source
1..610
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 6.91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR241536 (1-610)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
DB 86 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGACCTTG 130

RESULT 20

AR241537/c
LOCUS
DEFINITION
Sequence 82 from patent US 6471957. PAT 20-DEC-2002
ACCESSION
AR241537
VERSION
AR241537.1 GI:27287246
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 610)
AUTHORS
Sim,G.-K., Yang,S., Dreibitz,M.J. and Wonderling,R.S.
TITLE
Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL
Patent: US 6471957-A 82 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
EPX;

FEATURES

source
1..610
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 6.91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AR241537 (1-610)


```
Db 525 TTTCGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 481
|||||
RESULT 21
AR254492 LOCUS AR254492 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 80 from patent US 6482403.
ACCESSION AR254492
VERSION AR254492.1 GI:27303380
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 80 19-NOV-2002;
Heska Corporation; Fort Collins, CO
FEATURES
source
1..610
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 6,91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-787-382-20 (1-15) x AR254492 (1-610)
Qy 1 PheLaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
86 TTTCGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 130
|||||
RESULT 22
AR254493/c LOCUS AR254493 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 82 from patent US 6482403.
ACCESSION AR254493
VERSION AR254493.1 GI:27303381
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 82 19-NOV-2002;
Heska Corporation; Fort Collins, CO
FEATURES
source
1..610
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 6,91e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-787-382-20 (1-15) x AR254493 (1-610)
Qy 1 PheLaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
525 TTTCGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 481
|||||
```

```
RESULT 23
AF331920 LOCUS AF331920 1658 bp DNA linear MAM 04-OCT-2001
DEFINITION Canis familiaris interleukin-5 gene, complete cds.
ACCESSION AF331920
VERSION AF331920.1 GI:15919182
KEYWORDS
SOURCE
ORGANISM Canis familiaris (dog)
Canis familiaris
Canis familiaris
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 1658)
AUTHORS Yang,S., Sellins,K.S., Weber,E. and McCall,C.
TITLE Canine interon of interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein
JOURNAL J Interferon Cytokine Res. 21 (6), 361-367 (2001)
PUBMED 11440833
REFERENCE 2 (bases 1 to 1658)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA
FEATURES
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1..1658
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1..26
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/note="IL-5"
/codon_start=1
/product="interleukin-5"
/protein_id="AALI0716.1"
/db_xref="GI:15919183"
/translation="MRMLNLNLALGAAYVSFAVENPMNRLVAETITLTLSTHRTWL
IGDNLMIPTPENKHOLCIKEVFGIDITLKNQTAHGEAVDKLFQNLISLKHIERQK
KRCAGERWRVTKFLDYLVQVFLGVINTEWTPES"
1622..1658
3'UTR
ORIGIN
Alignment Scores:
Pred. No.: 2.2e-05 Length: 1658
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x AF331920 (1-1658)
Qy 1 PheLaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
84 TTTCGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 128
|||||
RESULT 24
ECU91947 LOCUS ECU91947 405 bp mRNA linear MAM 05-APR-1997
DEFINITION Equus caballus interleukin-5 (IL-5) mRNA, complete cds.
ACCESSION U91947
VERSION U91947.1 GI:1928883
KEYWORDS
SOURCE Equus caballus (horse)
Equus caballus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 405)
AUTHORS Vandergriff,E.V. and Horohov,D.W.
TITLE Equine interleukin-5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 405)
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/Note="clone overlaps with GenBank Accession Number
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/estimated_length=unknown
misc_feature 139083..172134
/Note="assembly_fragment
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vector_side:right"

ORIGIN
Alignment Scores:
Pred. No.: 1.13 Length: 172134
Score: 63.00 Matches: 13
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 14 Gaps: 0

US-10-787-382-20 (1-15) x AC158733 (1-172134)

Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
Db 129022 GCTGTAGAAAGTCTTATGATAGACTGGTGCAGAGACCTTG 128981

RESULT 26
AC158734 177136 bp DNA linear HTG 23-MAR-2005
LOCUS Rhinolophus ferrumequinum clone VMRC7-400D16, WORKING DRAFT
DEFINITION Rhinolophus ferrumequinum (greater horseshoe bat)
ACCESSION AC158734
VERSION AC158734.1 GI:61696377
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Rhinolophus ferrumequinum
ORGANISM Rhinolophus ferrumequinum (greater horseshoe bat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
Rhinolophidae; Rhinolophinae; Rhinolophus.
REFERENCE 1 (bases 1 to 177136)
AUTHORS Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Gestole,M., Greene,A., Guan,X., Gupta,J., Haghighi,P.,
Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G., Hurler,B., Idol,J.R.,
Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q., Legaspi,R.,
Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C., Puri,O.,
Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Sison,C.,
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Stephen,E., Tave,A., Thomas,J.W., Thomas,P.J.,
Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 177136)
Green,E.D.
Direct Submission
Submitted (23-MAR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: imh
Center clone name: 400D16
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175003 bases at least Q40

```

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Consensus quality: 175393 bases at least Q30
Consensus quality: 175604 bases at least Q20
Insert size: 219000; agarose-fp
Insert size: 176736; sum-of-contigs
Quality coverage: 8.73x in Q20 bases; agarose-fp
Quality coverage: 10.81x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 7760: contig of 7760 bp in length
* 7761 7860: gap of unknown length
* 7861 20486: contig of 12626 bp in length
* 20487 20586: gap of unknown length
* 20587 43544: contig of 22958 bp in length
* 43545 43644: gap of unknown length
* 43645 95366: contig of 51722 bp in length
* 95367 95466: gap of unknown length
* 95467 177136: contig of 81670 bp in length.
Location/Qualifiers
1..177136
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/mol_type="genomic DNA"
/db_xref="taxon:59479"
/clone="VMRC7-400D16"
/clone_lib="VMRC7"
/Note="BAC resource: http://bacpac.chori.org/"
1..7760
/Note="assembly_fragment
clone end:SP6
vector_side:right"
7761..7860
/estimated_length=unknown
7861..20486
/Note="assembly_fragment"
20487..20586
/estimated_length=unknown
20587..43544
/Note="assembly_fragment
clone end:other
vector_side:left"
43545..43644
/estimated_length=unknown
43645..95366
/Note="assembly_fragment"
95367..95466
/estimated_length=unknown
95467..177136
/Note="assembly_fragment"

ORIGIN
Alignment Scores:
Pred. No.: 1.17 Length: 177136
Score: 63.00 Matches: 13
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 92.86% Mismatches: 0
Query Match: 85.14% Indels: 0
DB: 14 Gaps: 0

US-10-787-382-20 (1-15) x AC158734 (1-177136)

Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
Db 101345 GCTGTAGAAAGTCTTATGATAGACTGGTGCAGAGACCTTG 101386

RESULT 27
AF051372 AF051372 354 bp mRNA linear MAM 26-JUL-2000
LOCUS

```

```

DEFINITION Felis catus Interleukin-5 mRNA, partial cds.
ACCESSION AF051372
VERSION AF051372.1 GI:2961560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Harley,R., Helps,C.R., Harbourn,D.A., Gruffydd-Jones,T.J. and Day,M.J.
TITLE Cytokine mRNA expression in lesions in cats with chronic gingivostomatitis
JOURNAL Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
PUBMED 10391845
REFERENCE
AUTHORS Harley,R., Day,M.J., Gruffydd-Jones,T.J., Harbourn,D.A. and Helps,C.R.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1998) Clinical Veterinary Science, Bristol University, Langford House, Langford, Bristol BS40 5DU, UK
FEATURES
source
1..354
/organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_line="FL4"
<1..>354
/notes="IL-5"
/codon_start=2
/product="interleukin-5"
/protein_id="AAC05752.1"
/db_xref="GI:2961561"
/translation="LGAAXVSAIAVQSPMNRVLVAETLLSTHRTLIGDGNLMITPTPEHNNHQLCIEEVFGQIDTLKNRTVPGDAVEKLFRLSLIKEHIDRQKNFGKWKVKNFLNLQPLFLGLNT"
ORIGIN
Alignment Scores:
Pred. No.: 0.00383 Length: 354
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 81.08% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x AF051372 (1-354)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 29 GCTGTACAAAGTCCCATGAATAGCTGGTGGCAGACCTTG 70

RESULT 28
AF068770
LOCUS AF068770
DEFINITION Felis catus interleukin 5 mRNA, complete cds.
ACCESSION AF068770
VERSION AF068770.1 GI:3342391
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Sylvain,H., Hughes,K.J. and O'Reilly,K.L.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-1998) VMP, LSU School of Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803, USA
REFERENCE
AUTHORS Vandegrift,E., Hughes,K.J. and O'Reilly,K.L.
TITLE Direct Submission

DEFINITION Felis catus Interleukin-5 mRNA, partial cds.
ACCESSION AF051372
VERSION AF051372.1 GI:2961560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Harley,R., Helps,C.R., Harbourn,D.A., Gruffydd-Jones,T.J. and Day,M.J.
TITLE Cytokine mRNA expression in lesions in cats with chronic gingivostomatitis
JOURNAL Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
PUBMED 10391845
REFERENCE
AUTHORS Harley,R., Day,M.J., Gruffydd-Jones,T.J., Harbourn,D.A. and Helps,C.R.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1998) Clinical Veterinary Science, Bristol University, Langford House, Langford, Bristol BS40 5DU, UK
FEATURES
source
1..354
/organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_line="FL4"
<1..>354
/notes="IL-5"
/codon_start=2
/product="interleukin-5"
/protein_id="AAC05752.1"
/db_xref="GI:2961561"
/translation="LGAAXVSAIAVQSPMNRVLVAETLLSTHRTLIGDGNLMITPTPEHNNHQLCIEEVFGQIDTLKNRTVPGDAVEKLFRLSLIKEHIDRQKNFGKWKVKNFLNLQPLFLGLNT"
ORIGIN
Alignment Scores:
Pred. No.: 0.00448 Length: 405
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 81.08% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x AF068770 (1-405)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GCTGTACAAAGTCCCATGAATAGCTGGTGGCAGACCTTG 102

RESULT 29
SSC010088
LOCUS SSC010088
DEFINITION Sus scrofa mRNA for interleukin-5.
ACCESSION AJ010088
VERSION AJ010088.2 GI:6911700
KEYWORDS IL-5 gene; interleukin-5.
SOURCE Sus scrofa (pig)
ORGANISM
REFERENCE
AUTHORS Sylvain,H., Matvienko,O., Leonchiks,A., Alving,K. and van der Ploeg,I.
TITLE Molecular cloning, expression, and purification of pig interleukin-5
JOURNAL Immunogenetics 51 (1), 59-64 (2000)
PUBMED 10663563
REFERENCE
AUTHORS Sylvain,H.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1998) Sylvain H., Department of Laboratory Medicine, Division of Clinical Immunology, Karolinska Institute/Karolinska Hospital, 171 76 Stockholm, SWEDEN
REMARK Revised by author
REFERENCE
AUTHORS Sylvain,H.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Sylvain H., Department of Laboratory Medicine, Division of Clinical Immunology, Karolinska Institute/Karolinska Hospital, 171 76 Stockholm, SWEDEN
COMMENT On Feb 7, 2000 this sequence version replaced gi:6782396.
FEATURES
source
1..405
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
1..405
/gene="IL-5"
JOURNAL Submitted (27-JUL-1998) VMP, LSU School of Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803, USA
REMARK Sequence update by submitter
COMMENT On Jul 28, 1998 this sequence version replaced gi:3201991.
FEATURES
source
1..405
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/mol_type="mRNA"
/db_xref="taxon:9685"
1..405
/codon_start=1
/product="interleukin 5"
/protein_id="AAC27616.1"
/db_xref="GI:3342392"
/translation="MRMLHLHLALGAAYVSAIAVQSPMNRVLVAETLLSTHRTLIGDGNLMITPTPEHNNHQLCIEEVFGQIDTLKNRTVPGDAVEKLFRLSLIKEHIDRQKNKCGGRWRVKFLDYQLQVFLGVINTEWTIES"
ORIGIN
Alignment Scores:
Pred. No.: 0.00448 Length: 405
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 81.08% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x AF068770 (1-405)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GCTGTACAAAGTCCCATGAATAGCTGGTGGCAGACCTTG 102

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CDS
1..405
/gene="IL-5"
/codon_start=1
/product="interleukin-5"
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/db_xref="GI:6911701"
/db_xref="GOA:Q9MYM5"
/db_xref="UniProt:IPR000186"
/translation="MRMLHLSLGLGAAVSAIAVENTMRLVAETLTLLSIHRTLL
IGDGNLMISTPVHTNHOLCIEEVFGIDTLKNQTARGDAVEKLFQNLSLIKEIDRQK
KNCGERVRVTFQLDYLVQVFLGVINTWTMES"

ORIGIN
Alignment Scores:
Pred. No.: 0.00448 Length: 405
Score: 60.00 Matches: 13
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 81.08% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x SSC010088 (1-405)

Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 61 GCTGTAGAAAATACCATGACTGTGGTGCAGAGACCTTG 102

RESULT 30
LOCUS SSC133452 529 bp mRNA linear MAM 15-APR-2005
DEFINITION Sus scrofa mRNA for interleukin 5.
ACCESSION AJ133452
VERSION AJ133452.2 GI:6967055
KEYWORDS IL-5 gene; interleukin 5.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1
AUTHORS Johnsen,C.K., Grondahl-Hansen,J., Johansen,R., Jungersen,G. and
Heegaard,P.M.H.
JOURNAL Sus scrofa mRNA for interleukin-5
REFERENCE 2
AUTHORS Johnsen,C.K.
JOURNAL Direct Submission
Submitted (02-MAR-1999) Johnsen C.K., Department of Biochemistry
and Immunology, Danish Veterinary Laboratory, Bulowsvej 27, DK-1790
Copenhagen V, DENMARK
REMARK revised by [3]
AUTHORS Johnsen,C.K.
JOURNAL Direct Submission
Submitted (07-FEB-2000) Johnsen C.K., Department of Biochemistry
and Immunology, Danish Veterinary Laboratory, Bulowsvej 27, DK-1790
Copenhagen V, DENMARK
COMMENT On Feb 11, 2000 this sequence version replaced gi:4469326.
FEATURES
Location/Qualifiers
1..529
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/cell_type="lymph node"
/tissue_type="lung"
1..529
/gene="IL-5"
1..405
/gene="IL-5"
/codon_start=1
/product="interleukin 5"
/protein_id="CAB38328.1"

CDS
1..405
/gene="IL-5"
/codon_start=1
/product="interleukin-5"
/protein_id="CAB70611.2"
/db_xref="GI:6911701"
/db_xref="GOA:Q9MYM5"
/db_xref="UniProt:IPR000186"
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IGDGNLMISTPVHTNHOLCIEEVFGIDTLKNQTARGDAVEKLFQNLSLIKEIDRQK
KNCGERVRVTFQLDYLVQVFLGVINTWTMES"

ORIGIN
Alignment Scores:
Pred. No.: 0.0104 Length: 838
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 81.08% Indels: 0

US-10-787-382-20 (1-15) x SSC133452 (1-529)

Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 61 GCTGTAGAAAATACCATGACTGTGGTGCAGAGACCTTG 102

RESULT 31
LOCUS AF025436 838 bp mRNA linear MAM 20-OCT-1998
DEFINITION Felis catus interleukin-5 (IL-5) mRNA, complete cds.
ACCESSION AF025436
VERSION AF025436.1 GI:3228518
KEYWORDS Felis catus (cat)
SOURCE Felis catus
ORGANISM Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
REFERENCE 1 (bases 1 to 838)
AUTHORS Padrig,P.A., Qin,Y., Wells,T.N., Solway,J. and Camoretti-Mercado,B.
JOURNAL Sequence and structural analysis of feline interleukin-5 cDNA
Am. J. Vet. Res. 59 (10), 1263-1269 (1998)
PUBMED 9781459
REFERENCE 2 (bases 1 to 838)
AUTHORS Padrig,P.A., Qin,Y., Wells,T.N.C., Solway,J. and
Camoretti-Mercado,B.
JOURNAL Direct Submission
Submitted (15-SEP-1997) Medicine, University of Chicago, 5841 S.
Maryland Avenue, Chicago, IL 60637, USA
FEATURES
Location/Qualifiers
1..838
/organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/cell_type="activated feline peripheral blood mononuclear
cells"
1..838
/gene="IL-5"
45..449
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KNCGERVRVTFQLDYLVQVFLGVINTWTMES"

ORIGIN
Alignment Scores:
Pred. No.: 0.0104 Length: 838
Score: 60.00 Matches: 12
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 81.08% Indels: 0

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DB:
US-10-787-382-20 (1-15) x AF025436 (1-838)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 105 GCTGTAGAAAGTCCCATGAATAGGCTGTGGCAGACCTTG 146

RESULT 32
BTINTLEUS
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BTINTLEUS
B.taurus mRNA for interleukin-5.
267872
267872.1 GI:1113120
interleukin-5.
Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS
Mertens,B., Gobright,B. and Seow,H.F.
TITLE
The nucleotide sequence of the bovine interleukin-5-encoding cDNA
JOURNAL
Gene 176 (1-2), 273-274 (1996)
PUBMED
8918267
REMARK
(sites)
2 (bases 1 to 405)
REFERENCE
AUTHORS
Mertens,B.E.
TITLE
Direct Submission
JOURNAL
Submitted (13-NOV-1995) MERTENS B.E., International Livestock
Research Institute (ILRI), Bovine immunology, Naivasha road,
NAIROBI, KENYA
FEATURES
source
1..405
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_type="lymphocytes"
/tissue_type="blood"
1..405
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/product="interleukin-5"
/protein_id="CAA91779.1"
/db_xref="GI:1113121"
/db_xref="GCA:P52173"
/db_xref="InterPro:IPR000186"
/db_xref="InterPro:IPR009079"
/translation="MRHLTLVALGAAVVCANAVESTWNRVLVAETLTLLSHRTLL
IGDNLMTPTQHTNHCLEEVFGQIDTLKNOTAQGDVAVKKIFQNLISLIKEYIDLQK
RCGGERWRVKQFLDYLVQVPLGINTWNTMES"
ORIGIN
Alignment Scores:
Pred. No.: 0.0535 Length: 405
Score: 55.00 Matches: 12
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 74.32% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x BTINTLEUS (1-405)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 61 GCTGTAGAAAGTCCCATGAATAGGCTGTGGCAGACCTTG 102

RESULT 33
OAUI3038
LOCUS
DEFINITION
ACCESSION
VERSION
OAUI3038
Ovis aries interleukin-5 mRNA, complete cds.
U35038
U35038.1 GI:4096663

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KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
REFERENCE
AUTHORS
1 (bases 1 to 520)
TITLE
Cloning of ovine interleukin-5 cDNA
JOURNAL
Unpublished (1995)
2 (bases 1 to 520)
REFERENCE
AUTHORS
Seow,H.-F.
TITLE
Direct Submission
JOURNAL
Submitted (30-AUG-1995) Heng-Fong Seow, Animal Health, CSIRO,
Corner of Flemington Rd and Park Drive, Melbourne, Vic 3052,
Australia
FEATURES
source
1..520
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/mol_type="mRNA"
/db_xref="taxon:9940"
46..444
/codon_start=1
/product="interleukin-5"
/protein_id="AAC99991.1"
/db_xref="GI:4096664"
/translation="MHLRLTLVALGAAVVCANAVESTWNRVLVAETLTLLSHRTLLIG
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CGGERWRVKQFLDYLVQVPLGINTWNTMES"
ORIGIN
Alignment Scores:
Pred. No.: 0.0716 Length: 520
Score: 55.00 Matches: 12
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 74.32% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x OAUI3038 (1-520)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 100 GCTGTAGAAAGTACCATGAATAGACTGTGTGGCAGACCTTG 141

RESULT 34
OAUI3038
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
REFERENCE
AUTHORS
1 (bases 1 to 1140)
TITLE
Structure of the sheep interleukin-5 gene
JOURNAL
Unpublished
2 (bases 1 to 1140)
REFERENCE
AUTHORS
Bryson,C.E.
TITLE
Direct Submission
JOURNAL
Submitted (08-NOV-1994) Claire E. Bryson, Department of Veterinary
Science, University of Melbourne, Flemington Rd., Parkville,
Victoria, 3052, Australia
FEATURES
source
1..1140
/organism="Ovis aries"
/mol_type="genomic DNA"
/db_xref="taxon:9940"

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CAAT_signal 339..347
/gene="IL5"
TATA_signal 389..395
/gene="IL5"
exon <470..607
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/number=1
exon 824..856
/gene="IL5"
/number=2

ORIGIN

Alignment Scores:
Pred. No.: 0.178 Length: 1140
Score: 55.00 Matches: 12
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 74.32% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x OAILV1 (1-1140)

QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
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|||||:::|||||

Db 524 GCTGTAGAAAGTACCATGATAGATGTTGGCAGACCTTG 565

RESULT 35
AC149665

LOCUS AC149665 197131 bp DNA linear MAM 31-JUL-2004
DEFINITION Bos taurus BAC CH240-60013 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence.
AC149665
AC149665.2 GI:50872219
HTG.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 197131)
Muzny, D., Metzker, M., Adams, C., Agbai, II, O., Allen, C., Alsbrooks, S., Archer, P., Aredondo, H., Bandarnaike, D., Bangura, L., Beltran, B., Beltran, R., Beraducci, A., Biswal, K., Blyth, P., Bonham, H., Buhay, C., Burch, P., Cadore, I., Canada, A., Cardenas, V., Carter, K., Cavazos, I., Chacko, J., Chahrouh, M., Chavez, D., Chen, A., Chen, G., Chen, R., Cheng, M.-T., Chu, J., Clerc, K., Cockrell, R., Coyle, M., Cree, A., Curry, S., Dai, W., Davila, M.L., Davis, C., Davy-Carroll, L., De And, C., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Dziuda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Fowler, G., Fu, E., Fuh, E., Garcia, A., Garcia, R., Garner, T., Gaskin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D., Gonzalez-Garay, M., Guevara, W., Holder, R., Haaland, W., Haebler, K., Hall, B., Hamid, H., Hamilton, K., Harbes, B., Harris, R., Havlak, P., Hawes, A., Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J., Hines, S., Hitchens, M., Hodgson, A., Hogues, M., Hollins, B., Howell, L.T., Hulyk, S., Hume, J., Ima, K., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S., Keys, T., Khan, Z., King, D., Kovar, C., Kowis, A., Kowis, C., Lara, F., Leal, S., Lee, K., Lee, S., LeGall, F.I., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y.-S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorenshew, L., Lozano, R., Luk, T., Madu, R., Maheshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., McClelland, H., McPherson, J., Mercadado, C., Milosavljevic, A., Minja, E., Morgan, M., Morris, S., Munitasa, M., Murray, D., Nazareth, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Nott, A., Nwaokemele, O., Obregon, M., Ochi-Okorie, C., Odeh, E., Okwuonu, G., Okwuonu, K., Parker, D., Pasternak, S., Patel, B., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Primus, E., Pu, L.-L., Puzo, M., Qin, X., Quinn, A., Quiroz, J., Rabata, D., Rachlin, E., Reigh, R., Ren, Y., Reuter, M., Richards, S., Rives, C., Rodriguez, F., Rojas, A., Ruiz, S.J., Sana, M., Sanders, W., Santibanez, J., Santos, R.,

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repeat_region /rpt family="(TTTA)n" complement(12982..13213)
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repeat_region /rpt family="Bov-tA2" 13521..13734
repeat_region /rpt family="Bov-tA1" 14293..14578
repeat_region /rpt family="CHR-2A" 14718..14815
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repeat_region /rpt family="MER102b" 19565..19653
repeat_region /rpt family="MLT1K" complement(19660..19862)
repeat_region /rpt family="Bov-tA3" complement(21061..21617)
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repeat_region /rpt family="AT_rich" 21841..22126
repeat_region /rpt family="BOV-A2" complement(22186..22227)
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repeat_region /rpt family="(TA)n" 23107..23134
repeat_region /rpt family="AT_rich" 23458..23485
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repeat_region /rpt family="L1_Art" 30031..30105
repeat_region /rpt family="MER91B" 30141..30298

Alignment Scores:
Pred. No.: 70.3 Length: 197131
Score: 55.00 Matches: 12
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 74.32% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x AC149665 (1-197131)

QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 20446 GCTGTAGAAAGTACCATGATAGACTGGTGCAGAGACCTTG 20487

RESULT 36
CR543861.14/c
WPCOMMENT

Sequence split into 36 fragments LOCUS CR543861 Accession CR543861

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CR543861_02	200001	310000
CR543861_03	300001	410000
CR543861_04	400001	510000
CR543861_05	500001	610000
CR543861_06	600001	710000
CR543861_07	700001	810000
CR543861_08	800001	910000
CR543861_09	900001	1010000
CR543861_10	1000001	1110000
CR543861_11	1100001	1210000
CR543861_12	1200001	1310000
CR543861_13	1300001	1410000
CR543861_14	1400001	1510000
CR543861_15	1500001	1610000
CR543861_16	1600001	1710000
CR543861_17	1700001	1810000
CR543861_18	1800001	1910000
CR543861_19	1900001	2010000
CR543861_20	2000001	2110000
CR543861_21	2100001	2210000
CR543861_22	2200001	2310000
CR543861_23	2300001	2410000
CR543861_24	2400001	2510000
CR543861_25	2500001	2610000
CR543861_26	2600001	2710000
CR543861_27	2700001	2810000
CR543861_28	2800001	2910000
CR543861_29	2900001	3010000
CR543861_30	3000001	3110000
CR543861_31	3100001	3210000
CR543861_32	3200001	3310000
CR543861_33	3300001	3410000
CR543861_34	3400001	3510000
CR543861_35	3500001	3598621

Continuation (15 of 36) of CR543861 from base 1400001 (CR543861 Acinetobacter sp. ADP1)

Alignment Scores:
Pred. No.: 702 Length: 110000
Score: 49.00 Matches: 10
Percent Similarity: 86.67% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 66.22% Indels: 0


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DB:                                     1          Gaps:                                0

US-10-787-382-20 (1-15) x CR543861_14 (1-110000)

Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
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Db      73554 TTTCAGTGAAGGTAACCACTTAACAGATTGCTTGACAGCCGTTA 73510

RESULT 37
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LOCUS      AF419552                1247 bp      mRNA      linear      PLN 15-NOV-2001
DEFINITION Arabidopsis thaliana At2g47020/F14M4.15 mRNA sequence.
ACCESSION  AF419552
VERSION     AF419552.1  GI:16930397
KEYWORDS   FLI CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 1247)
AUTHORS    Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Arabidopsis cDNA clones
REFERENCE  2 (bases 1 to 1247)
AUTHORS    Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (14-SEP-2001) Salk Institute Genomic Analysis Laboratory
(SiGnAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
COMMENT    Incomplete ORF.
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEN (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J., Bower,L.,
Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
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Percent Similarity: 90.00% Conservatve: 0
Best Local Similarity: 90.00% Mismatches: 1
Query Match:    63.51% Indels:      0
DB:             15      Gaps:      0

US-10-787-382-20 (1-15) x AF419552 (1-1247)

Qy      5 AsnProMetAsnArgLeuValAlaGluThr 14
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Db      519 AATCCCATGAACAGATTGGCAGCGAGACC 490

RESULT 38
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LOCUS      AC004411                106329 bp      DNA      linear      PLN 11-MAR-2002
DEFINITION Arabidopsis thaliana chromosome 2 clone F14M4 map C1C06C03,
complete sequence.
ACCESSION  AC004411
VERSION     AC004411.3  GI:20197133
KEYWORDS   HTG.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 106329)
AUTHORS    Rounsley,S.D., Lin,X., Kaul,S., Shee,T.P., Fujii,C.Y., Mason,T.M.,
Shen,M., Romning,C.M., Fraser,C.M., Somerville,C.R. and Venter,J.C.
Unpublished
REFERENCE  2 (bases 1 to 106329)
AUTHORS    Lin,X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE  3 (bases 1 to 106329)
AUTHORS    Town,C.D. and Kaul,S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598415.
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(AC007236:11525..16031)."
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repeat_region
complement(6162..6182)
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6464..7254
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CDS
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FICEQLTKGLNQHISSGSEVDGSESGEFTGHPMCEFCRPFYGDNELYTHMS
REHYTCHICQLKPGOYEYGYNDLEVFRSDHFLCEDETCLAKKFTVFOIEABLKI
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DARTYLEYKGYGLSHLVDMARLCPDQROKELIDTHNACLKGNKGKAVKVESSD
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/notes="synonym: F14M4.9"
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18867. .18897
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/translation="MSLYFLRLLCSVEGKYLIOETHDSTTRREDDDFKONSEIVECV
NFSCTMPILISGRGFMIEIDQGLSSFFPLVVEDDDVCSIEIRILETTEFTGDSAKQ
AMDFTHEIGWLLHRSKLGESDPNPGVPLIRFQWLIETFSMDREWCATVIRKLNMPFDG
AVGESSSNATLSLCELLHRAVRKNKSPKMWELRLYIPKOQRNSLFRPDAAGPAGLT
PLHIAAGDGSDEVLDALTEDPAMVGIENAKTCRSTGTTFEDYARLHGHSFYIHLIQ
RKINKKSTTDEHVNVNIPVSFDRQKPKSGPMASAEITQIPCKLCKHKLVIYGTTR
RSVAYPAMLNSMAIAAVCVVALLFKSCPEVLYVFPQFRELLEDYGS"
complement(21637. .22434)
/gene="At2g47070"
/notes="synonym: F14M4.10"
complement(join(<21637. .21904,21980. .>22434))
/gene="At2g47070"
complement(join(21637. .21904,21980. .22434))

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Alignment Scores:

Pred. No.: 1.82e+03 Length: 106329
Score: 47.00 Matches: 9
Percent Similarity: 90.00% Conservative: 0
Best Local Similarity: 90.00% Mismatches: 1
Query Match: 63.51% Indels: 0
DB: 15 Gaps: 0

US-10-787-382-20 (1-15) x AC004411 (1-106329)

Qy 5 AsnProMetAsnArgLeuValAlaGluThr 14

Db 39280 AATCCCATGACAGATTGCCAGCGAGACC 39309

RESULT 39
SC0939129/c

LOCUS SC0939129 292200 bp DNA linear BCT 16-APR-2005
DEFINITION Streptomyces coelicolor A3(2) complete genome; segment 26/29.
ACCESSION AL049485 AL049587 AL079355 AL138598 AL138667 AL138668
AL138977 AL353864 AL353870 AL356593 AL356812 AL645882
AL939129.1 GI:24418971

VERSION Streptomyces coelicolor A3(2)
KEYWORDS Streptomyces coelicolor A3(2)
SOURCE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
ORGANISM Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE 1

AUTHORS Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L.,
Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S.,
Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S.,
Rabinowitch, E., Rajandream, M.A., Rutherford, K., Rutter, S.,
Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S.,
Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrell, B.G.,
Parkhill, J. and Hopwood, D.A.
Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)

JOURNAL Nature 417 (6885), 141-147 (2002)

PUBMED 1200953

REFERENCE 2 (bases 1 to 292200)

AUTHORS Bentley, S.D.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk

COMMENT On or before Oct 29, 2002 this sequence version replaced
gi:20520762, gi:20520792, gi:20520672, gi:20520775, gi:20520777,
gi:20520778, gi:20520779, gi:20520776, gi:20520674.

FEATURES

source

1. 292200
/organism="Streptomyces coelicolor A3(2)"
/mol_type="genomic DNA"
/strain="A3(2)"
/db_xref="taxon:100226"

gene

58. 1089
/gene="SC06712"
/note="synonym: SC4C6.22"

CDS

58. 1089
/gene="SC06712"
/note="SC4C6.22, possible copper oxidase, len: 343 aa;
weakly similar to members of the multicopper oxidase
family e.g. to the N-terminus of SW:COFA_PSES8
(EMBL:M19930), CopA, Pseudomonas syringae copper
resistance protein A precursor (609 aa), fasta scores:
opt: 170 z-score: 188.4 E(): 0.0036, 27.3% identity in 205
aa overlap. Also weakly similar to the blood coagulation
factors which are structurally related to the multicopper
oxidases. Similar to the N-terminus of TR:O53858
(EMBL:AL022004) Mycobacterium tuberculosis hypothetical
protein (504 aa) (25.1% identity in 323 aa overlap).
Contains PS00079 Multicopper oxidases signature 1 and
PS00080 Multicopper oxidases signature 2 (the latter
suggesting copper-binding)"

/codon_start=1
/transl_table=11
/product="putative copper oxidase"
/protein_id="CAB45586.1"
/db_xref="GI:5139568"
/db_xref="GOA:Q9XAL8"
/db_xref="InterPro:IPR002355"
/db_xref="InterPro:IPR006311"
/db_xref="InterPro:IPR011706"
/db_xref="UniProt/TREMBL:Q9XAL8"
/translation="MDRRGFNRRLGCGAAATSLSTAPEVAGAAPAAKGITARTAPA
GGEVHLKMYAEKLADCGMGYFEGKASVPGPLIEVNEGDTLHLEFNTMDVRASLH
VHGLDISSDGTAMNKSDVEPGCTRTYTRTHKGRDDGTWRPGSAGYHYHHDVV
TEHGTGIRNGLYGVIVHRRKGDVLPDATHIVFNDMTINNRKPHGTDFEATVGDR
VEIYMTGHEYTHFMHGRWADNRGTILGTPDDPDPSPRVIDNKITGPADSGFQIIAG
EGVGAGAMWYHCHVQSHSDMGVGLFLVKPDGTIPGYEPHEHGATAKSGSGEPTG
GAAAEHEH"
521. 544
/gene="SC06712"
/note="repeat 7; 23 bp imperfect inverted repeat"
901. 963
/gene="SC06712"
/note="PS00079 Multicopper oxidases signature 1"
916. 951
/gene="SC06712"
/note="PS00080 Multicopper oxidases signature 2"
1276. 2334
/gene="SC06713"
/note="synonym: SC4C6.23"
1276. 2334
/gene="SC06713"
/note="SC4C6.23, probable lacI-family transcriptional
regulator, len: 352 aa; similar to many e.g. TR:O87590
(EMBL:AF086819), CelR, Thermomonaspora fusca
transcriptional regulator of cellulase genes (340 aa),
fasta scores; opt: 991 z-score: 1119.2 E(): 0, 51.9%
identity in 324 aa overlap. Similar to others from S.
coelicolor e.g. TR:O86795 (EMBL:AL031317) S. coelicolor
putative transcriptional regulator (355 aa) (36.3%
identity in 342 aa overlap). Contains Pfam matches to
entry PF00532 Peripla BP like, Periplasmic binding
proteins and LacI family and to entry PF00356 lacI,
Bacterial regulatory proteins, lacI family. Contains
probable helix-turn-helix motif at aa 9-30 (Score 2307,
+7.04 SD)"
/codon_start=1
/transl_table=11
/product="putative transcriptional regulator"
/protein_id="CAB45587.1"
/db_xref="GI:5139569"
/db_xref="GOA:Q9XAL7"
/db_xref="InterPro:IPR001761"
/db_xref="InterPro:IPR000843"
/db_xref="UniProt/TREMBL:Q9XAL7"
/translation="MTETGPRPTLEAVERGATVSRVNVNGHGVDRDALEVRVR
AVEELGYVNHARSLLVTRHQAVVAVAEPETRVFADPYFAQLRGISKELTAHDNQ
LVLLITGREDHARVGRYLAGGHVGLVFLSHLHDLPLGLVRSAGVPTVFGRPDWD
DGRDDVYVSDNRGGARSVHVLGALGRTHIAHTIGPLDQTSADRAGLRGDRVPGGA
GPGLVARGDFTSGGGERAMRELLDRCPGLDAVFAANDLTAAGALRVLRGRGRVDDV
AVVGFDDMLPVAEQTPDPLTTRQDIEGMRMLRLLLRGLDRRAADATDFAARTPT
AAPFGVLLPTTLVHRSTA"
1291. 1374
/gene="SC06713"
/note="Pfam match to entry PF00356 lacI, Bacterial
regulatory proteins, lacI family, score 39.70, E-value
9.4e-10"
1465. 2202
/gene="SC06713"
/note="Pfam match to entry PF00532 Peripla BP like,
Periplasmic binding proteins and LacI family, score
95.60, E-value 9.5e-25"
complement(2088. 2111)
/note="repeat 7; 23 bp imperfect inverted repeat"

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gene      complement(2440..3231)
/ gene="SCO6714"
/ note="synonym: SC4C6.24c"
CDS       complement(2440..3231)
/ gene="SCO6714"
/ note="SC4C6.24c, possible hydroxylase, len: 263 aa;
similar to TR:O55078 (EMBL:U50973) Streptomyces sp. strain
C5 daunomycin C-14 hydroxylase (275 aa), fasta scores;
opt: 422 z-score: 482.3 E(): 1.5e-19, 38.5% identity in
273 aa overlap. Similar to TR:O50527 (EMBL:AL009204)
S.coelicolor hypothetical protein (267 aa) (37.9% identity
in 253 aa overlap) and to (EMBL:AL049863), SC5H1.09c,
S.coelicolor possible hydroxylase (265 aa) (35.7% identity
in 258 aa overlap). Also similar to hypothetical proteins
from Mycobacterium tuberculosis and to Mycobacterium
tuberculosis 27.3 kDa MAB HBT7 reactive antigen
(EMBL:AJ007737) (260 aa) (36.7% identity in 264 aa
overlap)"
/ codon_start=1
/ trans_table=11
/ product="putative hydroxylase"
/ protein_id="CAB45588.1"
/ db_xref="GI:5139570"
/ db_xref="InterPro:IPR004360"
/ translation="MLTTPVFGAPNWLDTGTSLDGATSFYGLFGWFRSAGPEAG
GTAFFELDRIVAGGHTTEBQGPFSWTVYFQAPDRAAQAQSGEHGQVLYQPHDVM
DQGTWALADLAGLPGIWPQGRGLVTFQSGALCWVELHTADIAAAAYRAVLG
LRTSGVFGGSGYTCVNPAGEGSDAMFGGLVFLAEDPADTADAGWLPYFAVDDATA
VARTLGGTGVMPATDIEGVGRVARLDAPYGARFAVLPRPQQ"
RBS       complement(3239..3244)
/ note="possible RBS"
3425..3670
/ gene="SCO6715"
/ notes="synonym: SC4C6.25"
3425..3670
/ gene="SCO6715"
/ note="SC4C6.25, probable transcriptional regulator, len:
81 aa, similar to many transcriptional regulators (some
putative) from Streptomyces e.g. TR:O53963 (EMBL:X62287),
WhiB, S.coelicolor transcriptional regulator essential for
sporulation (87 aa), fasta scores; opt: 336 z-score: 452.7
E(): 5.7e-18, 61.1% identity in 72 aa overlap. Also
similar to e.g. TR:O69649 (EMBL:AL02212) Mycobacterium
tuberculosis putative regulatory protein (100 aa) (40.0%
identity in 75 aa overlap)"
/ trans_table=11
/ product="putative transcriptional regulator"
/ protein_id="CAB45589.1"
/ db_xref="GI:5139571"
/ db_xref="GOA:O9XAL5"
/ db_xref="UniProt/TrEMBL:O9XAL5"
/ translation="MTETTTAAPDLKQREALCAQTGGDFFPEPGSSVRDAKICAL
CPIRSCLSPALSDRRPVGWGLSEKERLALRTIP"
4003..4197
/ gene="SCO6716"
/ notes="synonym: SC4C6.26"
4003..4197
/ gene="SCO6716"
/ note="SC4C6.26, hypothetical protein, len: 64 aa; unknown
function, probable CDS suggested by positional base
preference, GC frame plot and amino acid composition"
/ codon_start=1
/ trans_table=11
/ product="hypothetical protein"
/ protein_id="CAB45590.1"
/ db_xref="GI:5139572"

Alignment Scores:
Pred. No.: 5.89e+03 Length: 292200
Score: 47.00 Matches: 8

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/ gene="SCO6714"
/ note="synonym: SC4C6.24c"
CDS       complement(2440..3231)
/ gene="SCO6714"
/ note="SC4C6.24c, possible hydroxylase, len: 263 aa;
similar to TR:O55078 (EMBL:U50973) Streptomyces sp. strain
C5 daunomycin C-14 hydroxylase (275 aa), fasta scores;
opt: 422 z-score: 482.3 E(): 1.5e-19, 38.5% identity in
273 aa overlap. Similar to TR:O50527 (EMBL:AL009204)
S.coelicolor hypothetical protein (267 aa) (37.9% identity
in 253 aa overlap) and to (EMBL:AL049863), SC5H1.09c,
S.coelicolor possible hydroxylase (265 aa) (35.7% identity
in 258 aa overlap). Also similar to hypothetical proteins
from Mycobacterium tuberculosis and to Mycobacterium
tuberculosis 27.3 kDa MAB HBT7 reactive antigen
(EMBL:AJ007737) (260 aa) (36.7% identity in 264 aa
overlap)"
/ codon_start=1
/ trans_table=11
/ product="putative hydroxylase"
/ protein_id="CAB45588.1"
/ db_xref="GI:5139570"
/ db_xref="InterPro:IPR004360"
/ translation="MLTTPVFGAPNWLDTGTSLDGATSFYGLFGWFRSAGPEAG
GTAFFELDRIVAGGHTTEBQGPFSWTVYFQAPDRAAQAQSGEHGQVLYQPHDVM
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LRTSGVFGGSGYTCVNPAGEGSDAMFGGLVFLAEDPADTADAGWLPYFAVDDATA
VARTLGGTGVMPATDIEGVGRVARLDAPYGARFAVLPRPQQ"
RBS       complement(3239..3244)
/ note="possible RBS"
3425..3670
/ gene="SCO6715"
/ notes="synonym: SC4C6.25"
3425..3670
/ gene="SCO6715"
/ note="SC4C6.25, probable transcriptional regulator, len:
81 aa, similar to many transcriptional regulators (some
putative) from Streptomyces e.g. TR:O53963 (EMBL:X62287),
WhiB, S.coelicolor transcriptional regulator essential for
sporulation (87 aa), fasta scores; opt: 336 z-score: 452.7
E(): 5.7e-18, 61.1% identity in 72 aa overlap. Also
similar to e.g. TR:O69649 (EMBL:AL02212) Mycobacterium
tuberculosis putative regulatory protein (100 aa) (40.0%
identity in 75 aa overlap)"
/ trans_table=11
/ product="putative transcriptional regulator"
/ protein_id="CAB45589.1"
/ db_xref="GI:5139571"
/ db_xref="GOA:O9XAL5"
/ db_xref="UniProt/TrEMBL:O9XAL5"
/ translation="MTETTTAAPDLKQREALCAQTGGDFFPEPGSSVRDAKICAL
CPIRSCLSPALSDRRPVGWGLSEKERLALRTIP"
4003..4197
/ gene="SCO6716"
/ notes="synonym: SC4C6.26"
4003..4197
/ gene="SCO6716"
/ note="SC4C6.26, hypothetical protein, len: 64 aa; unknown
function, probable CDS suggested by positional base
preference, GC frame plot and amino acid composition"
/ codon_start=1
/ trans_table=11
/ product="hypothetical protein"
/ protein_id="CAB45590.1"
/ db_xref="GI:5139572"

Alignment Scores:
Pred. No.: 5.89e+03 Length: 292200
Score: 47.00 Matches: 8

Percent Similarity: 84.62% Conservativity: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 63.51% Indels: 0
DB: 1 Gaps: 0

US-10-787-382-20 (1-15) x SCO939129 (1-292200)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 226504 TTGGCTTCGACACCCGCTGACCGCATGTCATCGAA 226466

RESULT 40
AF336001/c
LOCUS AF336001
DEFINITION Swine hepatitis E virus isolate NLSW20 nonstructural protein gene,
partial cds.
ACCESSION AF336001
VERSION AF336001.1 GI:18478438
KEYWORDS
SOURCE
ORGANISM
Swine hepatitis E virus
Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
Hepevirus.
REFERENCE 1 (bases 1 to 242)
AUTHORS van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
Vivo,A., Kooreman,M. and de Roda Husman,A.M.
TITLE Hepatitis E virus sequences in swine related to sequences in
humans, The Netherlands
JOURNAL Emerging Infect. Dis. 7 (6), 970-976 (2001)
PUBMED 11747723
REFERENCE 2 (bases 1 to 242)
AUTHORS van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
Husman,A.M.
DIRECT SUBMISSION
JOURNAL Submitted (05-JAN-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
Bilthoven, Utrecht 3720 BA, The Netherlands
FEATURES
Location/Qualifiers
source
1..242
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/isolate="NLSW20"
/db_xref="taxon:63421"
/map="125-366"
<1..>242
/ note="ORF1"
/ codon_start=3
/ product="nonstructural protein"
/ protein_id="AAL73170.1"
/ db_xref="GI:18478439"
/ translation="VRPPLSRVQTEILINMQPRLVFRPEVLWNHPIQRIHNELEQ
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ORIGIN

Alignment Scores:
Pred. No.: 2.57 Length: 242
Score: 46.00 Matches: 7
Percent Similarity: 84.62% Conservativity: 4
Best Local Similarity: 53.85% Mismatches: 2
Query Match: 62.16% Indels: 0
DB: 13 Gaps: 0

US-10-787-382-20 (1-15) x AF336001 (1-242)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 125 TTCATTGTGGATAACCGCTTGATAGCATGATCCAGAG 87

RESULT 41
AF148211
LOCUS AF148211
DEFINITION Sigmoodon hispidus interleukin-5 (IL-5) mRNA, complete cds.
ACCESSION AF148211
VERSION AF148211.1 GI:10334679

AF148211 448 bp mRNA linear ROD 17-NOV-2000
Sigmoodon hispidus interleukin-5 (IL-5) mRNA, complete cds.
AF148211.1 GI:10334679

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-787-382-20 (1-15) x AF148211 (1-448)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 74 TTTCGCTGTGGAGATCCCTATGACACCGGTAGTGAAGAGACCTTG 118
RESULT 42
AX250264
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1 Streptomyces cinnamonensis
Streptomyces cinnamonensis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomycetes.
1
Leadlay, P.F., Staunton, J. and O'Liynyk, M.C.
Polyketides and their synthesis
Patent: WO 0168867-A 4 20-SEP-2001;
Biotica Technology Limited (GB)
Location/Qualifiers
1 .13600
/organism="Streptomyces cinnamonensis"
/mol_type="unassigned DNA"
/db_xref="taxon:1900"

Sigmodon hispidus (hispid cotton rat)
Sigmodon hispidus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Cricetidae; Sigmodontinae; Sigmodon.
1 (bases 1 to 448)
Howard, S., Jacquet, A., Haumont, M., Daminet, V., Milican, F.,
Glineur, F. and Bollen, A.
Cloning, expression and purification of recombinant cotton rat
interleukin-5
Gene 257 (1), 149-155 (2000)
11054577
2 (bases 1 to 448)
Howard, S.
Direct Submission
Submitted (03-MAY-1999) Applied Genetics, Free University of
Brussels, rue de l'Industrie, 24, Nivelles 1400, Belgium
Location/Qualifiers
1 .448
/organism="Sigmodon hispidus"
/mol_type="mRNA"
/db_xref="taxon:42415"
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1 .448
/gene="IL-5"
/note="cytokine"
/codon_start=1
/product="interleukin-5"
/protein_id="AAG16722.1"
/db_xref="GI:10334680"
/translation="MRMLHLISILTLACWTFVAFIPMHTVVKETLIQLSTHALLTS
NETVLPTVTHKHOLCTGEIPRGIDILKNQTVGTETLFGNLSLKKYIDRQKEK
CGEERRRFRQLDYLOEFLVGMGTWTEH"

5.24 Length: 448
46.00 Matches: 10
80.00% Conservative: 2
66.67% Mismatches: 3
62.16% Indels: 0
9 Gaps: 0

/note="Nucleotides 90001 - 103600 of the monensin
biosynthetic gene cluster"
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-787-382-20 (1-15) x AX250264 (1-13600)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
Db 8150-TTCTCTGTGCACGACCGATGTCACGTCTGTGCGCGAA 8188
RESULT 43
AC014950
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1 .16535
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-787-382-20 (1-15) x AC014950 (1-16535)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAla 12
Db 15098-TTTCGCTGTGCACAAACCCATTAAACCGATTGATCGG 15133
RESULT 44
AB071139
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AB071139
Apis mellifera Ks-1 non-coding nuclear RNA.
AB071139
AB071139.1 GI:22138802
Apis mellifera (honey bee)
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;

16535 bp DNA linear HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
AC014950
AC014950
AC014950.1 GI:6436385
HTG, HTGS_PHASE2.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 16535)
Adams, M. and Venter, J.C.
Direct Submission
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210325 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
1 .16535
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"


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repeat_region /rpt_family="AT_rich"
repeat_region complement(21659..21739)
repeat_region /rpt_family="U6"
21783..22084
repeat_region /rpt_family="AluSx"
22169..22189
repeat_region /rpt_family="AT_rich"
22563..22605
repeat_region /rpt_family="AT_rich"
complement(22650..22941)
repeat_region /rpt_family="AluJo"
complement(23193..23347)
repeat_region /rpt_family="MER104"
23615..23837
repeat_region /rpt_family="MER113"
23838..24137
repeat_region /rpt_family="AluJb"
24138..24334
repeat_region /rpt_family="MER113"
24459..24760
repeat_region /rpt_family="AluSx"
complement(25531..25777)

```

```

Alignment Scores: 6.26e+03 Length: 201020
Pred. No.: 45.00 Matches: 7
Score: 83.33% Conserved: 3
Percent Similarity: 58.33% Mismatches: 2
Best Local Similarity: 62.16% Indels: 0
Query Match: 8 Gaps: 0
DB:

```

US-10-787-382-20 (1-15) x AC022809 (1-201020)

```

QY 3 ValGluAnProMetAsnArgLeuValAlaGluThr 14
Db 56734 ATAGAAACCCATTTAATGAATAATAGCTGAACT 56699

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RESULT 49

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AC164180 226575 bp DNA linear HTG 01-JUL-2005
LOCUS Bos taurus clone CH240-154E1, *** SEQUENCING IN PROGRESS ***, 27
DEFINITION unordered pieces.
ACCESSION AC164180
VERSION AC164180.3 GI:68300674
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Bos taurus (cow)
ORGANISM

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REFERENCE
AUTHORS Muzny, D., Marie, Metzker, M., Lee, A., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K.,
Pavokelmen, O., Okwuonu, G., Olarpunsaagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umant, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 226575)
Worley, K.C.
Direct Submission
Submitted (18-JUN-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 226575)
Cow Genome Sequencing Consortium.
Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2005 this sequence version replaced gi:67972682.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FIXF
Center clone name: CH240-154E1
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 215151 bases at least Q40
Consensus quality: 218498 bases at least Q30
Consensus quality: 221135 bases at least Q20
Estimated insert size: 222126; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

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Lorensuhsawa, L., Loulaesed, H., Lozado, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mamoud, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
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 Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstock, G. and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 249287)
 Worley, K. C.
 Direct Submission
 Submitted (21-MAY-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 249287)
 Cow Genome Sequencing Consortium.
 Direct Submission
 Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: FGOM
 Center clone name: CH240-105K16
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 236931 bases at least Q40
 Consensus quality: 239534 bases at least Q30
 Consensus quality: 241569 bases at least Q20
 Estimated insert size: 244133; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTES: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 32 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 2228: contig of 2228 bp in length
 2278: gap of 50 bp
 2279: contig of 4389 bp in length
 6668: gap of unknown length
 6767: gap of 1768 bp in length
 8535: contig of 398 bp
 8934: contig of 3891 bp in length
 12824: contig of 727 bp
 13551: gap of 2189 bp in length
 13552: contig of 501 bp
 13741: gap of 501 bp
 16241: gap of 501 bp
 16242: contig of 5024 bp in length
 21266: gap of 450 bp
 21715: contig of 9593 bp in length
 31308: contig of 50 bp
 31309: contig of 4576 bp in length
 35344: gap of 50 bp
 35935: gap of 50 bp
 35985: contig of 7433 bp in length
 43417: gap of 50 bp
 43418: contig of 3346 bp in length
 46813: gap of 50 bp
 46863: gap of 50 bp
 56291: contig of 9428 bp in length
 56341: gap of 50 bp
 56292: gap of 50 bp
 62039: contig of 5698 bp in length
 62089: gap of 50 bp
 62090: contig of 2219 bp in length
 64308: contig of 684 bp
 64309: gap of 50 bp
 97962: contig of 32975 bp in length
 98017: gap of 50 bp
 98018: contig of 2093 bp in length
 100110: gap of 50 bp
 100111: contig of 9355 bp in length
 109515: gap of 50 bp
 109565: gap of 50 bp
 133886: contig of 24321 bp in length
 134066: gap of 180 bp
 134067: contig of 5605 bp in length
 139721: gap of 50 bp
 139722: contig of 1255 bp in length
 140977: gap of 50 bp
 141026: gap of 50 bp
 143608: contig of 2582 bp in length
 143609: gap of 50 bp
 147495: contig of 3837 bp in length
 147496: gap of 50 bp
 155613: contig of 8068 bp in length
 155614: gap of 50 bp
 158659: contig of 3206 bp in length
 158664: gap of 50 bp
 158919: gap of 50 bp
 163118: contig of 4199 bp in length
 163119: gap of 50 bp
 210196: contig of 47028 bp in length
 210197: gap of 50 bp
 210246: gap of 50 bp
 225457: contig of 15210 bp in length
 225814: gap of 357 bp
 238083: contig of 12270 bp in length
 238183: gap of unknown length
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 239283: gap of unknown length
 241096: contig of 1813 bp in length
 241097: gap of unknown length
 241197: contig of 1405 bp in length
 242701: gap of unknown length
 242702: contig of 2711 bp in length
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 1. 249287
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"

FEATURES
source

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31309. .31358
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35935. .35984
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43418. .43467

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Alignment Scores:

Pred. No.:	8.046+03	Length:	249287
Score:	46.00	Matches:	8
Percent Similarity:	92.31%	Conservative:	4
Best Local Similarity:	61.54%	Mismatches:	1
Query Match:	62.16%	Indels:	0
DB:	14	Gaps:	0

US-10-787-382-20 (1-15) x AC161834 (1-249287)

QY 3 ValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 DB 233045 CTGGAAATCCCATGGCAGAGTGGTGGCTCAGACGTA 233007

Search completed: December 21, 2005, 18:08:13
 Job time : 3135 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2005, 14:31:31 ; Search time 401 Seconds
(without alignments)
249.303 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74
Sequence: 1 PAVENPMRLVAETL 15

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US10787382/runat.16122005.132436.8002/app.query.fasta.1.199
-DB=N_Geneseq -QFWT=fastap -SUPRTX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10787382 @CNC 1 1 727 @runat.16122005.132436.8002 -NCPU=3
-NO.MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 21.*
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14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	74	100.0	345	3	Aaz55550 Canine ma
3	74	100.0	345	3	Aaz55551 Canine ma
4	74	100.0	402	3	Aaz55548 Canine in

c	5	74	100.0	402	3	Aaz55549	Canine in
	6	74	100.0	405	4	Aaf74300	Canine in
	7	74	100.0	610	3	Aaz55546	Canine in
c	8	74	100.0	610	3	Aaz55547	Canine in
	9	60	81.1	838	3	Aaz44265	Porcine I
	10	55	74.3	399	2	Aat50756	Ovine II-
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c	15	43	58.1	2256	10	ADE54216	Ade54216 Human gen
	16	42	56.8	363	5	RAF67150	Novel hum
c	17	42	56.8	507	6	ABQ91289	Abq91289 M. capsul
c	18	42	56.8	14707	6	AAL53529	Aal53529 Genomic D
	19	42	56.8	73771	11	ACN44938	Acn44938 Human gen
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	21	41	55.4	250	10	ADE06664	Hepatitis
c	22	41	55.4	381	10	ACF68089	Acf68089 Photorhab
	23	41	55.4	924	12	ADO07799	Ado07799 Fly polyn
	24	41	55.4	941	4	ABL30155	Abi30155 Drosophil
	25	41	55.4	1545	13	ADT42017	Adt42017 Bacterial
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	27	41	55.4	2000	10	ACC61263	Acc61263 Gene sequ
c	28	41	55.4	2000	10	ADK63721	Adk63721 Disease t
	29	41	55.4	2442	10	ADE06713	Ade06713 ORF1 gene
	30	41	55.4	2941	4	ABL30154	Abi30154 Drosophil
c	31	41	55.4	3004	10	ADD93578	Adad93578 Arabidops
	32	41	55.4	5138	10	ADE06707	Ade06707 ORF1 gene
	33	41	55.4	6496	4	ABL30196	Abi30196 Drosophil
c	34	41	55.4	7230	10	ADE06697	Ade06697 Hepatitis
	35	41	55.4	7233	10	ADE06694	Ade06694 Hepatitis
c	36	41	55.4	10708	13	ADV41357	Adv41357 Rat cardi
	37	41	55.4	110000	10	ACF67367	07
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	40	41	55.4	110000	10	ACF65384	2
c	41	40	54.1	459	4	ABA26715	Abaz26715 Probe #51
	42	40	54.1	480	8	ACA43050	Acac43050 Prokaryot
c	43	40	54.1	567	4	ABA31096	Abaz31096 Probe #95
	44	40	54.1	569	12	ACH72974	Ach72974 Human gen
c	45	40	54.1	913	5	AAS73628	Aas73628 DNA encod
	46	40	54.1	2310	12	ADN12289	Adn12289 Nematode
c	47	40	54.1	2518	5	AAS73627	Aas73627 DNA encod
	48	40	54.1	2520	5	AAS73629	Aas73629 DNA encod
c	49	40	54.1	2591	11	ADM01809	Adm01809 Human CDN
	50	40	54.1	6692	4	ABL14942	Abi14942 Drosophil
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c	57	39	52.7	121	11	ADZ42577	Adz42577 Human gen
	58	39	52.7	563	9	ACH39654	Ach39654 Human toe
	59	39	52.7	673	12	ADQ17913	Adq17913 Human sof
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	70	39	52.7	806	10	ABT32844	Abt32844 Human tum
	71	39	52.7	806	11	ADL92734	Adl92734 Human bre
	72	39	52.7	806	11	ADL92748	Adl92748 Human bre
	73	39	52.7	806	12	ADE44024	Ade44024 Human CDN
	74	39	52.7	806	12	ADE44038	Ade44038 Human CDN
	75	39	52.7	934	12	ADM16745	Adm16745 PERS-P1-H
c	76	39	52.7	1171	4	AAI71121	Aai71121 Escherich
	77	39	52.7	1171	4	AAI71102	Aai71102 Shigella

78	39	52.7	1171	4	AA1711103	AA171103 Shigella	151	38	51.4	1061	14	ADZ62645	Adz62645 Murine D1
79	39	52.7	1171	4	AA1711101	AA171101 Shigella	152	38	51.4	1271	6	ABQ70445	Abq70445 Listeria
80	39	52.7	1282	13	ADR26676	ADR26676 Breast ca	153	38	51.4	1365	12	ADO2070	Ado2070 Transcrip
81	39	52.7	1287	4	AAL26569	AAL26569 Human bre	154	38	51.4	1413	13	ADR63039	Adr63039 Cotton cd
82	39	52.7	1330	12	ADJ40258	Adj40258 Plant CDN	155	38	51.4	1425	11	ABD04226	Abd04226 Pseudomon
83	39	52.7	1344	13	ADT19823	Adt19823 Plant CDN	156	38	51.4	1508	3	AAC33986	Aac33986 Arabidops
84	39	52.7	1461	10	ADH83102	Adh83102 Enterococ	157	38	51.4	1521	3	AAC45478	Aac45478 Arabidops
85	39	52.7	1557	4	ABL26135	Ab126135 Drosophil	158	38	51.4	1521	11	ABD11142	Abd11142 Pseudomon
86	39	52.7	1675	4	AH44337	Aha44337 Human par	159	38	51.4	1650	10	ADH83085	Adh83085 Enterococ
87	39	52.7	1675	12	ADJ36452	Adj36452 Human CDN	160	38	51.4	1656	11	ABD13654	Abd13654 Pseudomon
88	39	52.7	1680	10	ADF02784	Adf02784 Bacterial	161	38	51.4	1756	4	ABL16203	Ab16203 Bacillus
89	39	52.7	1764	8	ACA33288	Aca33288 Prokaryot	162	38	51.4	1888	6	ABK76946	Abk76946 Acetabularia
90	39	52.7	1941	3	AC76885	Ac76885 Human ORF	163	38	51.4	1992	4	AAA89274	Aaa89274 Arabidops
91	39	52.7	1980	11	ACN88622	Acn88622 Breast ca	164	38	51.4	2000	12	ADJ41296	Adj41296 Plant CDN
92	39	52.7	2000	8	ADA72666	Ada72666 Rice gene	165	38	51.4	2560	5	AAS90227	Aas90227 DNA encod
93	39	52.7	2073	2	AAT13639	Aat13639 ACNPV ORF	166	38	51.4	2583	11	ABD10937	Abd10937 Pseudomon
94	39	52.7	2096	4	AAH15238	Aah15238 Human CDN	167	38	51.4	2868	4	ABA89419	Ab89419 Escherich
95	39	52.7	2096	12	ADN04883	Adn04883 Antipsoi	168	38	51.4	3131	14	ACL64050	Ac164050 M. xanthu
96	39	52.7	2415	4	AAS2659	Aas2659 E. coli D	169	38	51.4	3618	11	ABD13701	Abd13701 Pseudomon
97	39	52.7	2415	8	ACA32695	Aca32695 Prokaryot	170	38	51.4	3674	4	AAH29718	Aah29718 S. cerevis
98	39	52.7	3475	9	ACH04168	Ach04168 Human CDN	171	38	51.4	4064	10	ADF60666	Adf60666 Mouse CLC
99	39	52.7	3743	6	ABN81321	Abn81321 Human mas	172	38	51.4	4602	13	ACN38320	Acn38320 Tumour-as
100	39	52.7	3780	3	AAZ39542	Aaz39542 Superheat	173	38	51.4	4764	4	ABL07752	Ab107752 Drosophil
101	39	52.7	3780	5	AAH87608	Aah87608 Pyrococcu	174	38	51.4	7536	10	ADE53812	Ad53812 Human pro
102	39	52.7	3843	2	ABL26134	Ab126134 Drosophil	175	38	51.4	7772	11	ACN92870	Acn92870 Breast ca
103	39	52.7	4888	2	AAH13244	Aah13244 Enterococ	176	38	51.4	7879	4	ABL16202	Ab116202 Drosophil
104	39	52.7	4888	6	ABS99039	Abs99039 Enterococ	177	38	51.4	8100	9	ABZ80918	Abz80918 Mouse Bel
105	39	52.7	4934	8	ACD13362	Ac13362 Human DNA	178	38	51.4	8509	4	AAI67035	Aai67035 Nucleotid
106	39	52.7	5598	8	ABZ36346	Abz36346 Human sec	179	38	51.4	8509	6	AAI67035	Aai67035 Nucleotid
107	39	52.7	5997	2	AAQ12188	Aaq12188 Odontoglo	180	38	51.4	8509	6	AAI67035	Aai67035 Nucleotid
108	39	52.7	6597	2	AAQ38106	Aaq38106 ORSV cDNA	181	38	51.4	11030	14	ADY18911	Ady18911 DNA encod
109	39	52.7	7644	12	ADQ22527	Adq22527 Human sof	182	38	51.4	26147	4	ABL11324	Ab111324 Drosophil
110	39	52.7	21784	10	AD62371	Ad62371 Human pro	183	38	51.4	2768	2	AAH13060	Aah13060 Enterococ
111	39	52.7	21784	10	ABX16008	Abx16008 Human nov	184	38	51.4	32768	6	ABS98855	Abs98855 Enterococ
112	39	52.7	21799	4	ABA07343	Ab07343 Human pan	185	38	51.4	64976	2	AAV21209_16	AAv21209_16 Mouse can
113	39	52.7	21799	4	AAH32770	Aah32770 Human Gen	186	38	51.4	7215	4	AAK6832	Aak6832 Human imm
114	39	52.7	29559	4	AAH59546	Aah59546 Propionib	187	38	51.4	83719	13	ABD32705	Abd32705 Mouse can
115	39	52.7	29559	8	ACF64475	Acf64475 Propionib	188	38	51.4	89378	12	ADN47591_20	Adn47591_20 Continuation (21 o
116	39	52.7	53332	6	AAH48890	Aah48890 Human Pft	189	38	51.4	89378	12	ADN47205_20	Adn47205_20 Continuation (21 o
117	39	52.7	53332	12	ADQ97534	Adq97534 Mouse can	190	38	51.4	89378	12	ADN47960_20	Adn47960_20 Continuation (21 o
118	39	52.7	75164	13	AD67061	Ad67061 Mouse can	191	38	51.4	110000	12	ADN46845_00	Adn46845_00 Continuation (2 of
119	39	52.7	94911	12	ADQ97846	Adq97846 Human can	192	38	51.4	110000	12	ADN46845_00	Adn46845_00 Continuation (2 of
120	39	52.7	98690	6	ABK12169	Abk12169 Human DNA	193	38	51.4	110000	12	ADN46123_00	Adn46123_00 Thermococ
121	39	52.7	110000	10	ACF5385_4	Continuation (5 of	194	38	51.4	110000	12	ADN46123_00	Adn46123_00 Thermococ
122	39	52.7	110000	10	ACF67367_33	Continuation (34 o	195	38	51.4	110000	12	ADN46123_00	Adn46123_00 Thermococ
123	39	52.7	110000	12	ADN46845_15	Continuation (16 o	196	38	51.4	110000	14	ADZ45062_03	Adz45062_03 Continuation (14 o
124	39	52.7	110000	12	ADN47591_05	Continuation (6 of	197	38	51.4	110000	14	ADZ45062_03	Adz45062_03 Continuation (14 o
125	39	52.7	110000	12	ADN46123_15	Continuation (16 o	198	38	51.4	174481	14	ADY75919	Ady75919 Mouse clo
126	39	52.7	110000	12	ADN47209_05	Continuation (6 of	199	38	51.4	188017	11	ACN45148	Acn45148 Mouse gen
127	39	52.7	110000	12	ADN46464_15	Continuation (16 o	200	37.5	50.7	317425	14	ABZ35720	Abz35720 L. pneumo
128	39	52.7	110000	12	ADN47960_05	Continuation (6 of	201	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
129	39	52.7	133894	2	AAT13635	Aat13635 ACNPV gen	202	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
130	38.5	52.0	2133	13	ADS56643	Ad56643 Bacterial	203	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
131	38	51.4	200	3	AAC12833	Aac12833 Human sec	204	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
132	38	51.4	219	13	ADV39621	Adv39621 Rat cardi	205	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
133	38	51.4	330	3	ACA44253	Aca44253 Arabidops	206	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
134	38	51.4	341	6	ABN22637	Abn22637 Human ORF	207	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
135	38	51.4	348	12	ADP94506	Adp94506 Cotton ex	208	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
136	38	51.4	425	13	ACF89243	Acf89243 Human SIR	209	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
137	38	51.4	476	6	ABL83730	Ab183730 Human ova	210	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
138	38	51.4	505	5	AAH81628	Aah81628 Human dif	211	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
139	38	51.4	505	10	ADE76200	Ad76200 Human M-3	212	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
140	38	51.4	635	3	AAC44219	Aac44219 Arabidops	213	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
141	38	51.4	666	8	ADA71070	Ada71070 Rice gene	214	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
142	38	51.4	747	5	AAF87549	Aaf87549 Rice genu	215	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
143	38	51.4	747	5	AAF87551	Aaf87551 Rice genu	216	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
144	38	51.4	756	6	ACA22808	Aca22808 Prokaryot	217	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
145	38	51.4	784	6	ABS77162	Abs77162 Frog embr	218	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
146	38	51.4	923	11	ACL33024	Ac133024 Rice abio	219	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
147	38	51.4	1035	13	AD742241	Adt42241 Bacterial	220	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
148	38	51.4	1044	14	ACL70182	Ac170182 M. xanthu	221	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
149	38	51.4	1045	14	ADW84072	Adw84072 MAP3K9 ma	222	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r
150	38	51.4	1056	11	ABD13513	Abd13513 Pseudomon	223	37.5	50.7	1187	2	AAQ64115	Aaq64115 Thermal r

224	37	50.0	531	13	ACN62188	Acn62188 Cotton gy	c	297	37	50.0	1906	4	ABA89379	Abas89379 Escherich
225	37	50.0	543	8	ABZ54155	ABZ54155 Aspergill	c	298	37	50.0	1945	10	ADB53890	ADB53890 Primary r
226	37	50.0	555	4	AAK92641	AAK92641 Human cDN	c	299	37	50.0	1976	5	AAF93822	AAF93822 Human cDN
227	37	50.0	555	12	ADL29068	ADL29068 3' end of	c	300	37	50.0	1976	14	ADY63154	ADY63154 Human clo
228	37	50.0	576	6	ABZ14403	ABZ14403 Arabidops	c	301	37	50.0	1989	13	ADS64016	ADS64016 Bacterial
229	37	50.0	576	8	ADA68274	ADA68274 Arabidops	c	302	37	50.0	1989	13	ADS63641	ADS63641 Bacterial
230	37	50.0	601	13	ACN52466	ACN52466 Cotton an	c	303	37	50.0	2000	8	ADA72109	ADA72109 Rice gene
231	37	50.0	603	5	AAF94164	AAF94164 Primer sp	c	304	37	50.0	2000	8	ADA72674	ADA72674 Rice gene
232	37	50.0	603	14	ADY63591	ADY63591 Human clo	c	305	37	50.0	2000	8	ADA71656	ADA71656 Rice gene
233	37	50.0	611	8	ABZ54724	ABZ54724 Aspergill	c	306	37	50.0	2000	11	ACL38104	ACL38104 Rice stre
234	37	50.0	615	13	ADS47911	ADS47911 Bacterial	c	307	37	50.0	2000	11	ACL37113	ACL37113 Rice stre
235	37	50.0	634	4	ABA89381	ABA89381 Escherich	c	308	37	50.0	2000	12	ADJ40987	ADJ40987 Plant cDN
236	37	50.0	693	8	ACA24591	ACA24591 Prokaryot	c	309	37	50.0	2024	6	ABQ76378	ABQ76378 S. cerevi
237	37	50.0	831	14	ACL72098	ACL72098 M. xanthu	c	310	37	50.0	2024	12	ADQ24593	ADQ24593 Human sof
238	37	50.0	833	2	AAQ25034	AAQ25034 Bovine RS	c	311	37	50.0	2199	10	ADC08389	ADC08389 Rice DNA
239	37	50.0	835	3	AAF09241	AAF09241 Fusarium	c	312	37	50.0	2206	14	ADV97739	ADV97739 cDNA sequ
240	37	50.0	835	13	ADU53282	ADU53282 Fusarium	c	313	37	50.0	2231	4	AAH99815	AAH99815 Human pro
241	37	50.0	835	14	ADZ91285	ADZ91285 Fusarium	c	314	37	50.0	2245	4	AAK82349	AAK82349 Human imm
242	37	50.0	936	6	ABK73208	ABK73208 Bacillus	c	315	37	50.0	2283	4	ABL20647	ABL20647 Drosophil
243	37	50.0	936	8	ACA32419	ACA32419 Prokaryot	c	316	37	50.0	2328	10	ADG45274	ADG45274 Mutant De
244	37	50.0	941	8	ACA49138	ACA49138 Prokaryot	c	317	37	50.0	2328	10	ADG45273	ADG45273 Mutant De
245	37	50.0	963	5	AAH67228	AAH67228 C. glutami	c	318	37	50.0	2328	10	ADG45275	ADG45275 Mutant De
246	37	50.0	1000	3	AAK57826	AAK57826 Arachidon	c	319	37	50.0	2328	10	ADG45276	ADG45276 Mutant De
247	37	50.0	1032	2	AAK94209	AAK94209 Bacillus	c	320	37	50.0	2328	10	ADG45277	ADG45277 Mutant De
248	37	50.0	1041	3	AAZ51712	AAZ51712 Burkholde	c	321	37	50.0	2328	10	ADG45278	ADG45278 Mutant De
249	37	50.0	1041	3	AAZ51713	AAZ51713 Burkholde	c	322	37	50.0	2328	10	ADG45272	ADG45272 Mutant De
250	37	50.0	1041	3	AAZ51715	AAZ51715 Burkholde	c	323	37	50.0	2328	12	ADOS8190	ADOS8190 DNA encod
251	37	50.0	1041	3	AAZ51714	AAZ51714 Burkholde	c	324	37	50.0	2328	12	ADN75087	ADN75087 Wild-type
252	37	50.0	1053	3	AAK75683	AAK75683 DNA encod	c	325	37	50.0	2328	12	ADN59849	ADN59849 Pyrococcu
253	37	50.0	1068	8	ACA23794	ACA23794 Prokaryot	c	326	37	50.0	2328	12	ADQ26670	ADQ26670 Mutant De
254	37	50.0	1134	5	AAK89404	AAK89404 DNA encod	c	327	37	50.0	2328	12	ADQ26669	ADQ26669 Mutant De
255	37	50.0	1149	3	AAZ53806	AAZ53806 Neisseria	c	328	37	50.0	2328	13	ADQ71146	ADQ71146 Pfu DNA p
256	37	50.0	1149	3	AAK08180	AAK08180 Fusarium	c	329	37	50.0	2328	14	ADY80957	ADY80957 Mutant De
257	37	50.0	1149	13	ADU52221	ADU52221 Fusarium	c	330	37	50.0	2331	2	AAQ50112	AAQ50112 Gene enco
258	37	50.0	1149	14	ADZ90224	ADZ90224 Fusarium	c	331	37	50.0	2333	4	ABL27378	ABL27378 Drosophil
259	37	50.0	1225	14	ADW61654	ADW61654 Pinus rad	c	332	37	50.0	2493	10	ABZ39948	ABZ39948 N. gonorr
260	37	50.0	1273	14	AEK67684	AEK67684 Rice geno	c	333	37	50.0	2517	13	ADT07246	ADT07246 Pfu DNA p
261	37	50.0	1329	13	ADT46354	ADT46354 Bacterial	c	334	37	50.0	2517	13	ADT07245	ADT07245 Pfu DNA p
262	37	50.0	1433	2	AAQ65397	AAQ65397 Elm C10:O	c	335	37	50.0	2526	13	ADT07230	ADT07230 Pfu DNA p
263	37	50.0	1433	2	AAQ92306	AAQ92306 Elm class	c	336	37	50.0	2526	13	ADT07229	ADT07229 Pfu DNA p
264	37	50.0	1433	2	AAK36108	AAK36108 Elm acyl-	c	337	37	50.0	2532	13	ADT07186	ADT07186 Pfu DNA p
265	37	50.0	1433	2	AAV15230	AAV15230 C10:0-ACP	c	338	37	50.0	2535	13	ADR25649	ADR25649 Breast ca
266	37	50.0	1484	3	AAK47540	AAK47540 Arabidops	c	339	37	50.0	2535	13	ADT07187	ADT07187 Pfu DNA p
267	37	50.0	1486	3	AAK40456	AAK40456 Arabidops	c	340	37	50.0	2564	5	AAK89190	AAK89190 DNA encod
268	37	50.0	1521	11	ABD02990	ABD02990 Pseudomon	c	341	37	50.0	2583	10	ADB62856	ADB62856 Human cDN
269	37	50.0	1524	4	AAK06034	AAK06034 Yeast cys	c	342	37	50.0	2655	4	ABL13062	ABL13062 Drosophil
270	37	50.0	1524	9	AAK59829	AAK59829 Yeast cys	c	343	37	50.0	2724	5	ABA15116	ABA15116 Human per
271	37	50.0	1524	10	ACC61802	ACC61802 Gene sequ	c	344	37	50.0	2864	4	AAK94275	AAK94275 Human ful
272	37	50.0	1531	12	ADK62743	ADK62743 Disease t	c	345	37	50.0	2864	12	ADL30875	ADL30875 Full leng
273	37	50.0	1531	12	ADK62743	ADK62743 Disease t	c	346	37	50.0	2955	5	AAH65842	AAH65842 C. glutami
274	37	50.0	1533	1	AAH82431	AAH82431 B cell di	c	347	37	50.0	2955	8	ACA00203	ACA00203 C. glutam
275	37	50.0	1534	2	AAK88013	AAK88013 Murine in	c	348	37	50.0	3062	3	AAZ87684	AAZ87684 Human G p
276	37	50.0	1596	4	AAH34605	AAH34605 Human col	c	349	37	50.0	3075	13	ADT07208	ADT07208 Pfu DNA p
277	37	50.0	1602	14	ABE28967	ABE28967 Pinus rad	c	350	37	50.0	3075	13	ADT07209	ADT07209 Pfu DNA p
278	37	50.0	1620	8	ACA19512	ACA19512 Pseudomon	c	351	37	50.0	3106	2	AAV70135	AAV70135 Pyruvate
279	37	50.0	1620	8	ACA19515	ACA19515 Prokaryot	c	352	37	50.0	3106	4	AAV70135	AAV70135 Pyruvate
280	37	50.0	1623	2	AAK714925	AAK714925 T cell re	c	353	37	50.0	3316	10	ADI02625	ADI02625 TufD codi
281	37	50.0	1623	2	AAV64062	AAV64062 Plasmid p	c	354	37	50.0	3360	2	AAK07285	AAK07285 Human cDN
282	37	50.0	1656	14	AEA10860	AEA10860 Magnaport	c	355	37	50.0	3370	3	AAA16630	AAA16630 Human sec
283	37	50.0	1656	14	AEA12337	AEA12337 DNA encod	c	356	37	50.0	3377	12	ADQ18296	ADQ18296 Human sof
284	37	50.0	1656	14	AEA14792	AEA14792 Sub-famil	c	357	37	50.0	3377	13	ADP24259	ADP24259 PRO poly
285	37	50.0	1674	11	ABD03041	ABD03041 Pseudomon	c	358	37	50.0	3389	10	ADB79882	ADB79882 Human put
286	37	50.0	1682	4	AAK71695	AAK71695 Human imm	c	359	37	50.0	3389	11	ADP65829	ADP65829 Human end
287	37	50.0	1682	4	AAK71694	AAK71694 Human imm	c	360	37	50.0	3389	11	ADP65751	ADP65751 Human SM-
288	37	50.0	1682	4	AAK71697	AAK71697 Human imm	c	361	37	50.0	3420	2	AAQ43965	AAQ43965 Pyrococcu
289	37	50.0	1761	3	AAK71697	AAK71697 Human imm	c	362	37	50.0	3420	2	AAQ43965	AAQ43965 Pyrococcu
290	37	50.0	1785	11	ABD02924	ABD02924 Pseudomon	c	363	37	50.0	3420	2	AAK17981	AAK17981 Pyrococcu
291	37	50.0	1812	5	AAK593842	AAK593842 DNA encod	c	364	37	50.0	3465	5	AAH67229	AAH67229 C. glutami
292	37	50.0	1821	4	ABL24609	ABL24609 Drosophil	c	365	37	50.0	3465	14	ABE13128	ABE13128 C. glutam
293	37	50.0	1851	13	ADT41607	ADT41607 Bacterial	c	366	37	50.0	3508	5	ADL63625	ADL63625 Human ova
294	37	50.0	1861	6	ABK75009	ABK75009 Bacillus	c	367	37	50.0	3575	12	ADQ87654	ADQ87654 Human tum
295	37	50.0	1887	8	ACA00696	ACA00696 C. glutam	c	368	37	50.0	3575	13	ADQ84415	ADQ84415 Human tum
296	37	50.0	1892	4	ABL20645	ABL20645 Drosophil	c	369	37	50.0	3595	10	ADJ87396	ADJ87396 DNA repli

370	37	50.0	3659	12	ADQ22831	Human sof	Adq22831 Human sof
371	37	50.0	4024	11	ACN88855	Breast ca	Acn88855 Breast ca
372	37	50.0	4056	4	ABL09821	Drosophila	Abi09821 Drosophila
373	37	50.0	4133	13	ACN42874	Human dia	Acn42874 Human dia
374	37	50.0	4158	10	ADG77045	Human nuc	Adg77045 Human nuc
375	37	50.0	4173	13	ADG92941	Mitogen-a	Adg92941 Mitogen-a
376	37	50.0	4190	4	ABL24608	Drosophila	Abi24608 Drosophila
377	37	50.0	4278	8	ACN33304	Prokaryot	Acn33304 Prokaryot
378	37	50.0	4320	10	ADH84843	Enterococ	Adh84843 Enterococ
379	37	50.0	4437	6	AA316840	Rat CIRL	Aa316840 Rat CIRL
380	37	50.0	4464	12	ADM97581	Human cal	Adm97581 Human cal
381	37	50.0	4497	10	ADC26274	Human NOV	Adc26274 Human NOV
382	37	50.0	4571	13	ADS10070	Human the	Ads10070 Human the
383	37	50.0	4675	8	AA049443	Human kin	Aad49443 Human kin
384	37	50.0	4687	12	ADQ24075	Human sof	Adq24075 Human sof
385	37	50.0	4707	2	AA770813	Deep Vent	Aat770813 Deep Vent
386	37	50.0	4707	2	AAV68142	DNA polym	Aav68142 DNA polym
387	37	50.0	4707	13	ADS11410	Human the	Ads11410 Human the
388	37	50.0	4780	11	ACN44533	Mouse mRN	Acn44533 Mouse mRN
389	37	50.0	4828	2	AAV70138	Pyruvate	Aav70138 Pyruvate
390	37	50.0	4928	4	AA723627	RutD/8 ge	Aaf23627 RutD/8 ge
391	37	50.0	4983	4	ABL03779	Drosophila	Abi03779 Drosophila
392	37	50.0	5008	8	ABX63351	Human cDN	Abx63351 Human cDN
393	37	50.0	5362	4	ABL04953	Drosophila	Abi04953 Drosophila
394	37	50.0	5439	6	ABL33402	Human imm	Abi33402 Human imm
395	37	50.0	5602	10	ABD58940	Toxicity-	Abd58940 Toxicity-
396	37	50.0	5602	10	ABD53676	Primary r	Abd53676 Primary r
397	37	50.0	5656	4	ABL10071	Drosophila	Abi10071 Drosophila
398	37	50.0	5758	4	ABL23284	Drosophila	Abi23284 Drosophila
399	37	50.0	5999	4	ABL13590	Drosophila	Abi13590 Drosophila
400	37	50.0	6279	8	ABT18891	Aspergill	Abt18891 Aspergill
401	37	50.0	6279	8	ABT20711	Aspergill	Abt20711 Aspergill
402	37	50.0	6330	8	ABT18297	Aspergill	Abt18297 Aspergill
403	37	50.0	6330	2	AA780113	Murine IL	Abt20113 Aspergill
404	37	50.0	6727	3	AA780113	Murine IL	Aat88014 Murine IL
405	37	50.0	6727	3	AA73648	Murine Int	Aac73648 Murine Int
406	37	50.0	6727	8	ABX04302	Mouse Int	Abx04302 Mouse Int
407	37	50.0	6727	12	ADR11379	Murine in	Adr11379 Murine in
408	37	50.0	7223	4	ABL03778	Drosophila	Abi03778 Drosophila
409	37	50.0	8330	8	ABT19517	Aspergill	Abt19517 Aspergill
410	37	50.0	8330	8	ABT17703	Aspergill	Abt17703 Aspergill
411	37	50.0	8614	4	AAK74343	Human imm	Aak74343 Human imm
412	37	50.0	8966	4	ABL20644	Drosophila	Abi20644 Drosophila
413	37	50.0	9325	14	ACL64440	M. xanthu	Abi20644 Drosophila
414	37	50.0	9889	4	ABL10070	Drosophila	Abi10070 Drosophila
415	37	50.0	11739	2	AAK13087	Enterococ	Aax13087 Enterococ
416	37	50.0	11739	6	ABS98882	Enterococ	Abs98882 Enterococ
417	37	50.0	12413	4	ABL20646	Drosophila	Abi20646 Drosophila
418	37	50.0	12619	5	AAH26493	Human low	Aah26493 Human low
419	37	50.0	15140	14	ABE11265	Bovine RS	Aeb11265 Bovine RS
420	37	50.0	15413	4	AAK84002	Human imm	Aak84002 Human imm
421	37	50.0	21844	5	ABA20799	Human ner	Aba20799 Human ner
422	37	50.0	22573	2	AAK37254	Human gen	Aax37254 Human gen
423	37	50.0	22671	2	AAV31200	E. coli J	Aav31200 E. coli J
424	37	50.0	28614	11	ACN44532	Mouse gen	Acn44532 Mouse gen
425	37	50.0	40433	6	ABN96830	Gene #332	Abn96830 Gene #332
426	37	50.0	42034	12	ADQ97373	Human can	Adq97373 Human can
427	37	50.0	52872	4	ABL04952	Drosophila	Abi04952 Drosophila
428	37	50.0	57763	9	ADA02528	Human MYB	Ada02528 Human MYB
429	37	50.0	57763	10	ADB72266	Human MYB	Adb72266 Human MYB
430	37	50.0	57763	10	ADB72266	Human MYB	Adb72266 Human MYB
431	37	50.0	90220	6	ABK33576	Human cDN	Abk33576 Human cDN
432	37	50.0	110000	2	AAZ02048	Continuation (8 of	Aaz02048 Continuation (8 of
433	37	50.0	110000	2	AAZ01425	Complete	Aaz01425 Complete
434	37	50.0	110000	11	ACN43984	Continuation (4 of	Acn43984 Continuation (4 of
435	37	50.0	110000	12	ADN46845	Continuation (19 o	Adn46845 Continuation (19 o
436	37	50.0	110000	12	ADN47591	Continuation (2 of	Adn47591 Continuation (2 of
437	37	50.0	110000	12	ADN46123	Continuation (19 o	Adn46123 Continuation (19 o
438	37	50.0	110000	12	ADN47209	Continuation (2 of	Adn47209 Continuation (2 of
439	37	50.0	110000	12	ADN46464	Continuation (19 o	Adn46464 Continuation (19 o
440	37	50.0	110000	12	ADN47960	Continuation (2 of	Adn47960 Continuation (2 of
441	37	50.0	168174	6	ABT11173	Human 5-1	Abt11173 Human 5-1
442	37	50.0	168273	6	ABT11114	Human 5-1	Abt11114 Human 5-1

ALIGNMENTS

RESULT 1
AAF74305

ID AAF74305 standard; DNA; 252 BP.

XX

AC AAF74305;

XX

DT 04-MAY-2001 (first entry)

XX

DE Canine interleukin-5 coding sequence #2.

XX

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;

```

KW inflammatory reaction; ds.
XX
XX Canis sp.
XX PN WO200111049-A2.
XX PD 15-FEB-2001.
XX
XX 09-AUG-2000; 2000WO-US021651.
XX
XX 10-AUG-1999; 99US-00371615.
XX PA (IDEX-) IDEXX LAB INC.
XX
XX Guo H, Lawton R, Mermer B, Aiyappa AP;
XX WPI; 2001-191542/19.
XX DR P-PSDB; AAB72616.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
XX generating antibodies which are useful in treating allergies in dogs.
XX
XX Example 1; Fig 1; 48pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
XX cancer and inflammatory reactions in dogs. The present sequence is one
XX version of the IL-5 coding sequence shown in the specification
XX
XX SQ Sequence 252 BP; 69 A; 54 C; 60 G; 69 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.37e-06 Length: 252
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x AAF74305 (1-252)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 58 TTTGCTGTAGAAATCCCATGATAGACTGTGGCAGACCTTG 102

RESULT 2
AAZ55550
ID AAZ55550 standard; cDNA; 345 BP.
XX
XX AAZ55550;
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine mature interleukin-5 (IL-5) cDNA.
XX
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1999; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX
XX DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX
XX P-PSDB; AAY58220.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 226-227; 264pp; English.
XX
XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting
XX
XX SQ Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.38e-06 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AAZ55550 (1-345)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 1 TTTGCTGTAGAAATCCCATGATAGACTGTGGCAGACCTTG 45

RESULT 3
AAZ55551/c
ID AAZ55551 standard; cDNA; 345 BP.
XX
XX AAZ55551;
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine mature interleukin-5 (IL-5) cDNA complement.
XX
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1999; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX
XX DR P-PSDB; AAY58220.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX
XX PT

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PT useful for treating or preventing e.g. tumors or autoimmune disease.
 XX Claim 1h; Page 226; 264pp; English.
 XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 9.38e-06 Length: 345
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AAZ55551 (1-345)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 Db 345 TTTCGTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 301

RESULT 4
 AAZ55548
 ID AAZ55548 standard; cDNA; 402 BP.
 XX AC AAZ55548;
 XX DT 14-MAR-2000 (first entry)
 XX DE Canine interleukin-5 (IL-5) cDNA coding region.
 XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX OS Canis familiaris.
 XX PN WO9961618-A2.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US011942.
 XX PR 29-MAY-1998; 98US-0087306P.
 XX PA (HESK-) HESKA CORP.
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI; 2000-072623/06.
 XX P-PSDB; AAY58219.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.
 XX Claim 1h; Page 225; 264pp; English.

XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 1.13e-05 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AAZ55548 (1-402)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 Db 58 TTTCGTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTG 102

RESULT 5
 AAZ55549/c
 ID AAZ55549 standard; cDNA; 402 BP.
 XX AC AAZ55549;
 XX DT 14-MAR-2000 (first entry)
 XX DE Canine interleukin-5 (IL-5) cDNA coding region complement.
 XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX OS Canis familiaris.
 XX PN WO9961618-A2.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US011942.
 XX PR 29-MAY-1998; 98US-0087306P.
 XX PA (HESK-) HESKA CORP.
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI; 2000-072623/06.
 XX P-PSDB; AAY58219.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.
 XX Claim 1h; Page 226; 264pp; English.
 XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or

CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targetting

SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.13e-05 Length: 402
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AA255549 (1-402)

Qy 1 PheAlaValGluAenPrometAsnArgLeuValAlaGluThrLeu 15
 Db 345 TTTGCTGTAGAAATCCCATGATAGACTGTGGCAGACCTTG 301

RESULT 6
 AAF74300
 ID AAF74300 standard; DNA; 405 BP.

XX AC AAF74300;

XX DT 04-MAY-2001 (first entry)

XX DE Canine interleukin-5 coding sequence #1.

XX KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 XX inflammatory reaction; ds.

XX OS Canis sp.

XX PN WO20011049-A2.

XX PD 15-FEB-2001.

XX PF 09-AUG-2000; 2000WO-US021651.

XX PR 10-AUG-1999; 98US-00371615.

XX PA (INDEX-) IDEXX LAB INC.

XX PI Guo H, Lawton R, Mermer B, Aiyappa AP;

XX DR WPI; 2001-191542/19.

XX DR P-PSDB; AAB72615.

XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs.

XX PS Claim 31; Page 46; 48pp; English.

XX CC The present invention provides the protein and coding sequences of the
 XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 XX cancer and inflammatory reactions in dogs. The present sequence is one
 XX version of the IL-5 coding sequence shown in the specification

SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.14e-05 Length: 405
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x AAF74300 (1-405)

Qy 1 PheAlaValGluAenPrometAsnArgLeuValAlaGluThrLeu 15
 Db 58 TTTGCTGTAGAAATCCCATGATAGACTGTGGCAGACCTTG 102

RESULT 7

AAZ55546

ID AAZ55546 standard; cDNA; 610 BP.

XX AC AAZ55546;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX FH Key Location/Qualifiers

XX CDS 29..433

XX FT /*tag= a

XX FT /product= "Canine IL-5"

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1h; Page 223-224; 264pp; English.

XX CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
 XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 XX nucleotides which encode these immunoregulatory proteins. The proteins,
 XX their associated nucleic acids, specific antibodies and inhibitors may be
 XX used as vaccines for therapeutic or prophylactic regulation of an immune
 XX response in animals (particularly cats, dogs, horses and humans). They
 XX may be used to treat autoimmune or infectious diseases including
 XX allergies, tumours, inflammation and graft rejection, and to increase the
 XX response from a co-administered antigen. The nucleotide sequences can
 XX also be used for the recombinant production of a protein, while
 XX nucleotide fragments are useful as probes, as amplification primers and
 XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 XX The proteins may be used to raise antibodies and to screen for modulators
 XX of activity, while the antibodies may be used in detection, and in drug

CC targetting
 XX Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;
 SQ Alignment Scores:
 Pred. No.: 1.89e-05 Length: 610
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AA255546 (1-610)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 DB 86 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGACCTTG 130

RESULT 8
 AA255547/C
 ID AA255547 standard; cDNA; 610 BP.
 AC AA255547;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-5 (IL-5) cDNA complement.
 XX
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT CDS complement(178..582)
 FT /*tag= a
 FT /product= "Canine IL-5"
 XX
 PN WO961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US011942.
 XX
 PR 29-MAY-1998; 98US-0087306P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dretz MJ, Wonderling RS;
 XX
 DR WPI; 2000-072623/06.
 DR P-PSDB; AAY58219.
 XX

Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease.
 Claim 1h; Page 224-225; 264pp; English.

Sequences AA255546-Z55551 represent cDNA sequences encoding canine
 interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 nucleotides which encode these immunoregulatory proteins. The proteins,
 their associated nucleic acids, specific antibodies and inhibitors may be
 used as vaccines for therapeutic or prophylactic regulation of an immune
 response in animals (particularly cats, dogs, horses and humans). They
 may be used to treat autoimmune or infectious diseases including
 allergies, tumours, inflammation and graft rejection, and to increase the
 response from a co-administered antigen. The nucleotide sequences can
 also be used for the recombinant production of a protein, while
 nucleotide fragments are useful as probes, as amplification primers and
 as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for modulators
 of activity, while the antibodies may be used in detection, and in drug
 CC targetting
 XX
 SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.89e-05 Length: 610
 Score: 74.00 Matches: 15
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x AA255547 (1-610)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 DB 525 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGACCTTG 481

RESULT 9
 AA244265
 ID AA244265 standard; DNA; 838 BP.
 XX
 AC AA244265;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Porcine IL-5 DNA.
 XX
 KW Pig; vaccine; cysticercosis; protective antigen; CC1; CC3; CC4;
 KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
 XX
 OS Sus scrofa.
 XX
 PN CN1231339-A.
 XX
 PD 13-OCT-1999.
 XX
 PF 29-JAN-1999; 99CN-00113447.
 XX
 PR 29-JAN-1999; 99CN-00113447.
 XX
 PA (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.
 XX
 PI Sun S, Dai J;
 XX
 DR WPI; 2000-087904/08.
 XX
 PT Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
 XX
 PS Claim 3; Page 9; 21pp; Chinese.

This invention describes a novel nucleic acid vaccine for preventing and
 curing human and pork cysticercosis. The invention involves the formation
 of a eukaryotic expression plasmid from fusion transcript expression unit
 consisting of three protective antigen genes (CC1, CC3 and CC4) of pig
 tenial cysticercus and coexpression unit of related cell factor gamma
 interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The
 CC induction and purification process of said nucleic acid vaccine is
 simple and convenient, the physical and chemical properties of the
 CC vaccine are stable, and the vaccine is easy to store and transport, and
 CC possesses effective immunological protective function for human and pig
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the
 CC method of the invention

SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.0211 Length: 838
 Score: 60.00 Matches: 12
 Percent Similarity: 100.00% Conservatives: 2
 Best Local Similarity: 85.71% Mismatches: 0

Query Match:	81.08%	Indels:	0
DB:	3	Gaps:	0
US-10-787-382-20 (1-15) x AAZ44265 (1-838)			
QY	2 AlavaiGluAsnProMetAsnArgIeuValAlaGIuThrLeu 15		
DB	105 GCTGTACAAAGTCCCATGATGAATAGGCTGGTGGCAGACCTTG 146		
RESULT 10			
ID	AAT50756 standard; cDNA; 399 BP.		
XX	AAT50756;		
AC	XX		
DT	17-OCT-2003 (revised)		
DT	24-SEP-1997 (first entry)		
XX	XX		
DE	Ovine IL-5 cDNA.		
XX	XX		
KW	Cytokine; ovine; sheep; interleukin-5; interleukin-12;		
KW	livestock; cow; stress; transport; vaccine adjuvant; ve		
KW	immunosuppression; allergy; reproductive system; growth		
KW	antibody; diagnosis; immunopotentiator;		
KW	early haematopoietic progenitor cell; cytotoxic cell; t		
XX	secretion; IgM; IgA; bacterial endotoxin; gamma-interfe		
XX	XX		
OS	Ovis aries.		
XX	XX		
PN	WO9700321-A1.		
XX	XX		
PD	03-JAN-1997.		
XX	XX		
PF	14-JUN-1996; 96WO-AU000360.		
XX	XX		
PR	14-JUN-1995; 95AU-00003502.		
PR	27-OCT-1995; 95AU-00006244.		
XX	XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
XX	XX		
PI	Seow H, Wood P;		
XX	XX		
DR	WPI; 1997-077528/07.		
DR	P-PSDB; AAW08479.		
XX	XX		
PT	Nucleic acid encoding ovine interleukin-5 or -12 - used		
PT	adjuvants and to treat or prevent microbial infections		
XX	XX		
PS	Claim 6; Page 41-42; 78pp; English.		
XX	XX		
CC	The sequences given in AAT50755-56 encode ovine interle		
CC	Ovine IL-5 or IL-12 are used to treat and/or prevent in		
CC	livestock (esp. cows and sheep), particularly where the		
CC	addressed, e.g. during transport, IL-5 and IL-12 can als		
CC	adjuvants in vaccines for veterinary use (partic. weakl		
CC	subunit or synthetic peptide vaccines). They may also b		
CC	cancer, immunosuppression and allergy, to enhance/suppr		
CC	reproductive system and to promote growth or early matur		
CC	interleukin can be delivered from constructs or deliver		
CC	antibodies are useful in enzyme immunoassays for rapid		
CC	infection. The interleukins are immunopotentiators, esp		
CC	promotes growth of early haematopoietic progenitor cell		
CC	of cytotoxic cells from thymocytes, also it stimulates		
CC	secretion of IgM and IgA (in synergism with bacterial e		
CC	induces production of gamma-interferon by, and prolifer		
CC	cells and increases the (non)-specific cytolytic lympho		
CC	genetic constructs can also be used for in vitro produ		
CC	12. (Updated on 17-OCT-2003 to standardise OS field)		
XX	XX		
SQ	Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	0.0903	Length:	399

Score:	55.00	Matches:	12
Percent Similarity:	92.86%	Conservative:	1
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	74.32%	Indels:	0
DB:	2	Gaps:	0
US-10-787-382-20 (1-15) x AAT50756 (1-399)			
Qy	2 AlaVaIGluAsnProMetAenArgLeuValAlaGluThrLeu 15		
Db	55 GCTGTGAAGTACCACTGAATAGACTGGTGGCAGACCTTG 96		
RESULT 11			
AD	AAT50755		
ID	AAT50755 standard; DNA; 520 BP.		
AC	AAT50755;		
XX			
DT	17-OCT-2003 (revised)		
DT	24-SEP-1997 (first entry)		
XX			
DE	Ovine IL-5 gene.		
XX			
KW	Cytokine; ovine; sheep; interleukin-5; interleukin-12;		
KW	livestock; cow; stress; transport; vaccine adjuvant; growth		
KW	immunosuppression; allergy; reproductive system; growth		
KW	antibody; diagnosis; immunopotentiator;		
KW	early haematopoietic progenitor cell; cytotoxic cell;		
KW	secretion; IgM; IgA; bacterial endotoxin; gamma-interfer		
XX			
OS	Ovis aries.		
XX			
Key	Location/Qualifiers		
FT	46..444		
CDS	/tag= a		
FT	/product= "Ovine_IL-5"		
FT	46..183		
FT	/tag= b		
FT	/number= 1		
FT	184..216		
FT	/tag= c		
FT	/number= 2		
FT	217..345		
FT	/tag= d		
FT	/number= 3		
FT	346..480		
FT	/tag= e		
FT	/number= 4		
XX			
XX	WO9700321-A1.		
XX			
XX	03-JAN-1997.		
PD			
XX			
PF	14-JUN-1996; 96WO-AU000360.		
XX			
PR	14-JUN-1995; 95AU-00003502.		
PR	27-OCT-1995; 95AU-00006244.		
XX			
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
XX			
PI	Seow H, Wood P;		
XX			
XX	WPI; 1997-077528/07.		
DR	P-PSDB; AAW08479.		
XX			
XX			
XX	Nucleic acid encoding ovine interleukin-5 or -12 - used		
FT	adjuvants and to treat or prevent microbial infections		
XX			
PS	Claim 6; Page 39-40; 78pp; English.		
XX			
CC	The sequences given in AAT50755-56 encode ovine interleukin		
CC	Ovine IL-5 or IL-12 are used to treat and/or prevent in		
CC	livestock (esp. cows and sheep), particularly where the		

stressed, e.g. during transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for veterinary use (partic. weakly immunogenic subunit or synthetic peptide vaccines). They may also be used to treat cancer, immunosuppression and allergy, to enhance/suppress the reproductive system and to promote growth or early maturity. Optionally interleukin can be delivered from constructs or delivery cells and antibodies are useful in enzyme immunoassays for rapid diagnosis of infection. The interleukins are immunopotentiators, especially IL-5 promotes growth of early haematopoietic progenitor cells and generation of cytotoxic cells from thymocytes, also it stimulates production and secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12 induces production of gamma-interferon by, and proliferation of, T and NK cells and increases the (non-)specific cytolytic lymphocyte response. The genetic constructs can also be used for in vitro production of IL-5 or -12. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.125 Length: 520
Score: 55.00 Matches: 12
Percent Similarity: 92.86% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 1
Query Match: 74.32% Indels: 0
DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x AAT50755 (1-520)

QY 2 AlaValGluAAsnProMetAenArgLeuValAlaGluThrLeu 15
|||||:::
DB 100 GCTGTAGAAAGTACCATGAATAGACTGGTGGCAGACCTTG 141

RESULT 12

ABX04971
ID ABX04971 standard; DNA; 103599 BP.

XX AC ABX04971,

XX DT 16-JAN-2003 (first entry)

XX S. cinnamomensis monensin type I polyketide synthase gene cluster.

XX Monensin; gene; cluster; polyketide synthase; antibiotic; ds;
KW antihelminthic; insecticide; immunosuppressant; antifungal;
KW antibacterial; polyether; mon BI; mon BII; mon CI; mon CII; mon HI;
KW mon RI; mon RII; mon T; mon AIX; mon AX.

XX Streptomyces cinnamomensis.

XX WO200168867-A1.

XX PD 20-SEP-2001.

XX PF 30-MAY-2000; 2000WO-GB002072.

XX PR 28-MAY-1999; 99GB-00012563.

XX PA (BIOT-) BIOTICA TECHNOLOGY LTD.

XX PI Leadlay PF, Staunton J, Oliynyk M;

XX WPI; 2001-611393/70.

DR P-PSDB; ABG99854, ABG99855, ABG99856, ABG99857, ABG99858, ABG99859,
DR ABG99860, ABG99861, ABG99862, ABG99863, ABG99864, ABG99865, ABG99866,
DR ABG99867, ABG99868, ABG99869, ABG99870, ABG99871, ABG99872, ABG99873,
DR ABG99874, ABG99875, ABG99876, ABG99877, ABG99878, ABG99879, ABG99880,
DR ABG99881, ABG99882, ABG99883, ABG99884, ABG99885, ABG99886, ABG99887.

PT New DNA sequence encoding polyketide synthase, useful for the production
PT of polyketides such as antibiotic monensin.

XX Claim 1; Page 116-195; 212pp; English.

XX

CC The invention relates to a DNA sequence which is a fully defined sequence
CC of 103551 base pairs appearing as ABX04971, or its variant, that it is
CC not a sequence encoding all or part amino acids 1-920 encoded by mon AI
CC as given in the specification. The DNA is the S. cinnamomensis polyketide
CC antibiotic monensin biosynthetic gene cluster. Also included are a
CC recombinant cloning or expression vector comprising the gene cluster, a
CC transformed host cell which has been transformed to contain the gene
CC cluster (and is capable of expressing a corresponding polypeptide), a
CC hybridization probe derived from the gene cluster (for identification and
CC isolation of the same or analogous gene cluster, e.g. one which binds
CC specifically to a region of the monensin gene cluster selected from mon
CC BI, mon BII, mon CI, mon CII, mon HI, mon RII, mon RIII, mon T, mon AIX and
CC mon AX), the use of the mon RI gene or variant and a monensin promoter to
CC control expression of a heterologous gene in Streptomyces cinnamomensis,
CC a polypeptide encoded by a portion of the monensin gene cluster
CC (preferably comprising mon BI, mon BII, mon AIX or mon AX or their
CC mutants, alleles or variants), an epoxide synthase encoded by mon CI, a
CC cytochrome P-450 encoded by mon CII, producing S. cinnamomensis capable of
CC enhanced levels of production of monensin comprising engineering it to
CC overexpress the mon RI gene, S. cinnamomensis containing multiple copies
CC of the mon RI gene and/or its variants, expressing a gene heterologous to
CC S. cinnamomensis comprising transforming S. cinnamomensis with DNA
CC encoding a heterologous gene and expressing the gene under control of the
CC activator gene mon RI or actII/orf4 and 13-propyl erythromycin A. The
CC processes and materials (enzyme systems, nucleic acids and vectors) are
CC useful for preparing polyketides by recombinant synthesis. The
CC polyketides are useful as insecticides, antibiotics, antihelminthics,
CC antifungals, antibacterials or other pharmaceuticals. In particular the
CC gene is useful for the production of monensin, an antibiotic polyether
CC polyketide. The present sequence represents the monensin gene cluster
XX
XX Sequence 103599 BP; 13980 A; 37023 C; 37799 G; 14795 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 6.01e+03 Length: 103599
Score: 46.00 Matches: 9
Percent Similarity: 84.62% Conservative: 2
Best Local Similarity: 69.23% Mismatches: 2
Query Match: 62.16% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x ABX04971 (1-103599)

QY 1 PheAlaValGluAAsnProMetAenArgLeuValAlaGlu 13
|||||:::
DB 98149 TTCTCTGTGCACAGCCGATGTCACGTCTGGTCGCCGA 98187

RESULT 13

ADP69744/C

ID ADP69744 standard; DNA; 312477 BP.

XX AC ADP69744;

XX DT 09-SEP-2004 (first entry)

XX DE Human ROCK 1 DNA #2.

XX ds; gene; human; ROCK 1; hyperproliferative disorder; cancer.

XX OS Homo sapiens.

XX PN US2004115641-A1.

XX PD 17-JUN-2004.

XX PF 11-DEC-2002; 2002US-00317883.

XX PR 11-DEC-2002; 2002US-00317883.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Cowsett LM, Dobie KW;

XX

DR WPI; 2004-449381/42.
XX New oligonucleotide compound that inhibits expression of ROCK 1, useful
PT for preparing a composition for treating hyperproliferative disorder,
PT e.g., cancer.
XX
XX Example 15; SEQ ID NO 11; 195pp; English.
XX
XX The invention relates to a new compound, targeted to a nucleic acid
CC encoding ROCK 1, that specifically hybridizes with the nucleic acid
CC encoding ROCK 1 and inhibits expression of ROCK 1. The oligonucleotide
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorder, e.g. cancer. The present sequence represents
CC human ROCK 1 DNA.
XX
XX Sequence 312477 BP; 92110 A; 58460 C; 60155 G; 98196 T; 0 U; 3556 Other;
SQ
Alignment Scores:
Pred. No.: 2.34e+04 Length: 312477
Score: 46.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 62.16% Indels: 0
DB: 12 Gaps: 0
US-10-787-382-20 (1-15) x ADP69744 (1-312477)
Qy 3 ValGluAenProMetAsnArgLeuValAlaGluThr 14
Db 102920 ATAGAAAACCCATTTTAAATGAATAATAGCTGAACT 102885
RESULT 14
ID ABA97721
ID ABA97721 standard; cDNA; 673 BP.
XX ABA97721;
AC ABA97721;
XX
XX 28-JUN-2002 (first entry)
XX
XX Pepper mild mottle virus envelope gene cDNA.
XX
XX Pepper mild mottle virus; PMMV; envelope; Tobamovirus; transgenic plant;
KW plant expression vector; transgenic; gene; ss.
XX
XX Pepper mild mottle virus.
OS
FH Key Location/Qualifiers
FT CDS 1..480
FT /*tag= a
FT /product= "PMMV envelope protein"
XX
XX KR149216-BI.
XX
XX 17-AUG-1998.
PD
XX
XX 11-NOV-1994; 94KR-00029486.
PF
XX
XX 11-NOV-1994; 94KR-00029486.
PR
XX
XX (POHA-) POHANG ENG COLLEGE.
PA
XX
XX Nam H, Choe J, Lee H, Park Y, Kim C;
PI
XX
XX WPI; 2000-252824/22.
DR
XX
XX P-FSDB; ABB08908.
DR
XX
XX ENVELOPE GENE OF PEPPER MILD MOTTLE VIRUS.
PT
XX
XX Claim 1; Page 7; 12pp; Korean.
PS
XX
XX The invention relates to the envelope gene (ABA97721) and protein
CC (ABB08908) from pepper mild mottle virus (PMMV - a member of the
CC Tobamovirus family of single-stranded RNA viruses). The invention also
CC

CC encompasses plant expression vectors which comprise the PMMV envelope
CC gene. The present sequence represents cDNA encoding the PMMV envelope
CC protein
XX
XX Sequence 673 BP; 178 A; 141 C; 173 G; 181 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 50.3 Length: 673
Score: 43.00 Matches: 9
Percent Similarity: 69.23% Conservative: 0
Best Local Similarity: 69.23% Mismatches: 4
Query Match: 58.11% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-20 (1-15) x ABA97721 (1-673)
Qy 3 ValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
Db 289 GTAGAAAATCCGCAAAATCTTACAACTGCCGAGCGCTT 327
RESULT 15
ID ADE54216/c
ID ADE54216 standard; DNA; 2256 BP.
XX
XX ADE54216;
AC ADE54216;
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Human gene NM_005006, SEQ ID NO 19.
DE
XX
XX Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX
XX WO2003016475-A2.
FN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR
XX
XX 01-NOV-2001; 2001US-0346382P.
PR
XX
XX 26-NOV-2001; 2001US-0333347P.
PR
XX
XX (GEHO) GEN HOSPITAL CORP.
PA
XX
XX (FARB) BAYER AG.
XX
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX
XX WPI; 2003-268312/26.
DR
XX
XX GENBANK; NM_005006.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a

CC gene expression assays of M. capsulatus genes. The sequences shown in
 CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
 CC invention

SQ Sequence 507 BP; 60 A; 160 C; 180 G; 107 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 57 Length: 507
 Score: 42.00 Matches: 8
 Percent Similarity: 75.00% Conservatives: 1
 Best Local Similarity: 66.67% Mismatches: 3
 Query Match: 56.76% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x ABQ91289 (1-507)

Oy 3 ValGluAsnProMetAsnArgLeuValAlaGluThr 14
 |||||:::|||||
 DB 440 GTCAGAAATCCGGTGACAGGTGTGCGCGGAAACC 405

RESULT 18
 AAL53529/c
 ID AAL53529 standard; DNA; 14707 BP.
 XX AC AAL53529;
 XX DT 30-JAN-2003 (first entry)
 XX DE Genomic DNA of mouse EHD1 gene, SEQ ID No 3.
 XX KW Cytostatic; osteopathic; recombinant Eps15 homology; EH domain; EHD1;
 KW EHD2; endocytosis; IGF1 signaling; suppressing adhesion; invasion;
 KW metastasis; bone formation; osteoporosis; mouse; murine; gene; ds.
 XX OS Mus sp.
 XX PN US2002115069-A1.
 XX PD 22-AUG-2002.
 XX PF 17-MAY-1999; 99US-00312762.
 XX PR 21-FEB-1997; 97IL-00120283.
 XX PR 20-FEB-1998; 98US-00026898.
 XX PA (HORO/) HOROWITZ M.
 XX PA (MINT/) MINTZ L.
 XX PI Horowitz M, Mintz L;
 XX WPI; 2002-731288/79.
 XX Novel recombinant Eps15 homology domain containing protein useful for
 PT regulating endogenous EHD protein by regulating insulin-like growth
 PT factor 1 receptor cell signaling via altered clathrin coated pit mediated
 PT endocytosis.
 XX Claim 6; Page 32-39; 88pp; English.

The invention relates to a novel recombinant Eps15 homology (EH) domain
 containing protein 1 or 2 (EHD1 or EHD2) with an N-terminal region
 containing a nucleotide binding consensus site, a central coiled coil
 structure and a C-terminal region including an EH domain, where the
 polypeptide participates in endocytosis. The peptides, peptide analogues
 and/or the polynucleotide sequences are useful for regulating EHD1/2
 protein activity in vivo, where the EHD1/2 protein and its gene are
 useful for upregulating the protein activity. The novel method is useful
 for lowering the rate of IGF1 signaling and therefore useful for
 suppressing adhesion, invasion and metastasis where EHD is overexpressed,
 and therefore endocytosis. The method is also useful for elongating IGF1
 effects and therefore for increasing bone formation in osteoporosis
 conditions. This polynucleotide sequence represents the genomic DNA of a
 mouse EHD1 gene of the invention

XX SQ Sequence 14707 BP; 3397 A; 3826 C; 3894 G; 3568 T; 0 U; 22 Other;

Alignment Scores:
 Pred. No.: 3.61e+03 Length: 14707
 Score: 42.00 Matches: 8
 Percent Similarity: 69.23% Conservatives: 1
 Best Local Similarity: 61.54% Mismatches: 4
 Query Match: 56.76% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x AAL53529 (1-14707)

Oy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
 |||||:::|||||
 DB 12589 GCTGACAGACATCTATGACCAGATTAAACAATGGAACC 12551

RESULT 19
 ACN44938
 ID ACN44938 standard; DNA; 73771 BP.
 XX AC ACN44938;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human genomic sequence hCG37394.
 XX KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
 XX OS Homo sapiens.
 XX PN WO2003073826-A2.
 XX PD 12-SEP-2003.
 XX PF 28-FEB-2003; 2003WO-US006235.
 XX PR 01-MAR-2002; 2002US-00087192.
 XX PA (SAGR-) SAGRES DISCOVERY.
 XX PI Morris DW;
 XX WPI; 2003-328604/31.
 XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.
 XX Claim 1; SEQ ID NO 1636; Opp; English.

The present invention relates to novel DNA and protein sequences which
 are associated with carcinomas. The sequences are useful for: (i) for
 screening drug candidates; (ii) for screening of bioactive agent capable
 of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 a bioactive agent capable of modulating the activity of CAP; (iv) for
 evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
 (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 determining Carcinoma Associated (CA) gene copy number. In addition, the
 CA genes are useful as DNA vaccines and the CAP are useful as markers of
 carcinoma including lymphoma. The present sequence is one such CA coding
 sequence. Note: This patent is an equivalent to basic patent
 US200218586A1, for which no sequence data was published

XX SQ Sequence 73771 BP; 20930 A; 14938 C; 16429 G; 21180 T; 0 U; 294 Other;

Alignment Scores:
 Pred. No.: 2.63e+04 Length: 73771
 Score: 42.00 Matches: 8
 Percent Similarity: 69.23% Conservatives: 1
 Best Local Similarity: 61.54% Mismatches: 4
 Query Match: 56.76% Indels: 0

PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Duchaud E, Teourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 6556; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 381 BP; 105 A; 75 C; 96 G; 105 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 64.4 Length: 381
Score: 41.00 Matches: 8
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 53.33% Mismatches: 5
Query Match: 55.41% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x ACP68089 (1-381)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
DB 262 TTTCGATAGTAAGTAATCCACTGACCGCGGAGTCTCTTAACCTTG 306

RESULT 23
ADO07799
ID ADO07799 standard; cDNA; 924 BP.
XX
AC ADO07799;
XX
DT 01-JUL-2004 (first entry)
XX
DE Fly polynucleotide #58.
XX
KW Fly; gene; ss; fat cell number; fat cell size; obesity; diabetes;
KW anorectic; antidiabetic.
XX
OS Diptera.
XX
PN US2004071700-A1.
XX
PD 15-APR-2004.

XX 09-OCT-2002; 2002US-00267502.
XX
PR 09-OCT-2002; 2002US-00267502.
XX
PA (LIFE-) LIFE SCI DEV CORP.
XX
PI Kim J, Galant R;
XX
DR WPI; 2004-328526/30.
DR P-PSDB; ADO08016.
XX
PT Identifying compounds that influence fat cell number or size for treating
PT or preventing obesity or diabetes by exposing the cell to the agent and
PT identifying fat cell number or size relative to cells not exposed to the
PT agent.
XX
PS Claim 1; SEQ ID NO 125; 275pp; English.
XX
CC The invention relates to a method of identifying compounds that influence
CC fat cell number or size comprising providing a cell that expresses a gene
CC and an agent, exposing the cell to the agent and identifying fat cell
CC number or size relative to cells not exposed to the agent. The method
CC also comprises providing an expression vector and an agent, exposing the
CC vector to the agent, detecting a change in expression of the gene
CC relative to expression of the gene in an expression vector not exposed to
CC the agent, treating a subject with the agent and identifying fat cell
CC number or size in the subject. The agent comprises an antisense
CC oligonucleotide. The subject comprises a mammal, preferably a human. The
CC method also comprises providing a polypeptide and an agent, exposing the
CC polypeptide to the agent, detecting binding of the agent to the
CC polypeptide or a change in an activity of the polypeptide, treating a
CC subject with the agent and identifying fat cell number or size in the
CC subject. The agent comprises an antibody. A method of regulating fat cell
CC number or size comprises providing a subject containing fat cells and an
CC agent that changes the expression of a gene, and treating the subject
CC with the agent under conditions so that fat cell size or number in the
CC subject is altered. The method is useful for identifying compounds that
CC influence fat cell number or size, for preparing a composition for
CC treating or preventing obesity or diabetes. This sequence represents fly
CC cDNA used in the scope of the invention.
XX
SQ Sequence 924 BP; 232 A; 254 C; 269 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 192 Length: 924
Score: 41.00 Matches: 9
Percent Similarity: 64.29% Conservative: 0
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 55.41% Indels: 0
DB: 12 Gaps: 0

US-10-787-382-20 (1-15) x ADO07799 (1-924)
QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
DB 175 GCTGTGAGAAATCCCGACCGGACTCACTCTGGAACACTT 216

RESULT 24
ABL30155
ID ABL30155 standard; DNA; 941 BP.
XX
AC ABL30155;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41938.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX

```

PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX PF
XX 23-MAR-2000; 2000US-0191637P.
XX PR
XX 11-JUL-2000; 2000US-00614150.
XX PR
XX (PEXE ) PE CORP NY.
XX PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX PI
XX WPI; 2001-656860/75.
XX DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX PT
XX Claim 1; SEQ ID NO 41938; 21pp + Sequence Listing; English.
XX PS
XX The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 941 BP; 234 A; 259 C; 272 G; 176 T; 0 U; 0 Other;
XX SQ
Alignment Scores:
Pred. No.: 196 Length: 941
Score: 41.00 Matches: 9
Percent Similarity: 64.29% Conservative: 0
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 55.41% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x ABL30155 (1-941)
QY 2 AlaValGluAsnProMetAnArgLeuValAlaGluThrIeu 15
Db 192 GCTGTGAGAAATCCCGACGCGACTCACTGTGGAACACTT 233
RESULT 25
ADT42017
ID ADT42017 standard; cDNA; 1545 BP.
XX
XX ADT42017;
XX AC
XX 02-DEC-2004 (first entry)
XX DT
XX Bacterial polynucleotide #16768.
XX DE
XX Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
XX OS
XX US2003233675-A1.
XX PN
XX 18-DEC-2003.
XX PD
XX 20-FEB-2003; 2003US-00369493.
XX PF
XX
XX 21-FEB-2002; 2002US-0360039P.
XX PR
XX (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX PI
XX WPI; 2004-061375/06.
XX DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PT
XX Claim 1; SEQ ID NO 40455; 122pp; English.
XX PS
XX The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polynucleotide used in
XX CC the scope of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1545 BP; 220 A; 601 C; 525 G; 199 T; 0 U; 0 Other;
XX SQ
Alignment Scores:
Pred. No.: 361 Length: 1545
Score: 41.00 Matches: 8
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 55.41% Indels: 0
DB: 13 Gaps: 0
US-10-787-382-20 (1-15) x ADT42017 (1-1545)
QY 2 AlaValGluAsnProMetAnArgLeuValAlaGluThrIeu 15
Db 1153 GCCGAGGACAAATCCGATCAACGCTGCTGGCCCGCACCTG 1194
RESULT 26
ABZ16494/C
ID ABZ16494 standard; DNA; 1798 BP.
XX
XX ABZ16494;
XX AC
XX 21-JAN-2003 (first entry)
XX DT
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 4299.
XX DE
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX KW
XX Arabidopsis thaliana.
XX OS

```


CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 2941 BP; 835 A; 629 C; 698 G; 779 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 798 Length: 2941
Score: 41.00 Matches: 9
Percent Similarity: 64.29% Conservative: 0
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 55.41% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x ABL30154 (1-2941)

Qy 2 AlaValGluuAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 1192 GCTGTGAGAAATCCCGACCGCGACTCACTGTGGAACACTT 1233

RESULT 31

ID ADD93578/c
XX ADD93578 standard; DNA; 3004 BP.

AC ADD93578;

DT 29-JAN-2004 (first entry)

DE Arabidopsis pathogen-inducible promoter P26.

KW Promoter; plant; pathogen resistance; transgenic; crop protection;
KW disease resistance; ds.

OS Arabidopsis thaliana.

PN WO2003083042-A2.

XX 09-OCT-2003.

XX 24-OCT-2002; 2002WO-US034220.

PR 24-OCT-2001; 2001US-0335249P.

PA (DNAP) DNA PLANT TECHNOLOGY CORP.

PI Repetti P., Scofield SR, Century K;

XX WPI; 2003-779453/73.

XX New isolated nucleic acid molecule useful for enhancing resistance of a
PT plant to a pathogen (e.g. bacteria, viruses, fungi, nematodes or
PT insects).

PS Claim 7; Page 29-30; 41pp; English.

XX The present sequence is that of a pathogen-inducible promoter, denoted
CC P26, of Arabidopsis thaliana. Pathogen-inducible promoters were
CC identified in an experiment in which gene expression in wild-type Col-0
CC Arabidopsis plants was monitored over the course of a Botrytis cinerea
CC infection. Genes were identified whose expression was up-regulated during
CC pathogen infection compared to uninfected tissue, and promoter sequences
CC were isolated by PCR amplification. The promoters can be used to enhance
CC pathogen resistance in plants, e.g. by being operably linked to a
CC resistance effector gene.

SQ Sequence 3004 BP; 989 A; 582 C; 466 G; 967 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 819 Length: 3004
Score: 41.00 Matches: 6
Percent Similarity: 80.00% Conservative: 6
Best Local Similarity: 40.00% Mismatches: 3

Query Match: 55.41% Indels: 0
DB: 10 Gaps: 0
US-10-787-382-20 (1-15) x ADD93578 (1-3004)

Qy 1 PheAlaValGluuAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 2964 TTTAATATAGAAATCCCTCGCACATTAATTAACAACAGTA 2920

RESULT 32

ADE06707/c

ID ADE06707 standard; DNA; 5138 BP.

XX ADE06707;

AC ADE06707;

DT 29-JAN-2004 (first entry)

DE ORF1 gene from Hepatitis E virus strain JRAL.

KW ds; gene; hepatitis E virus; chips; kit; detection.

XX Hepatitis E virus; strain JRAL.

XX Key Location/Qualifiers

FT CDS 27..5138

FT /*tag= a

XX WO2003000887-A1.

XX 03-JAN-2003.

XX 25-JUN-2002; 2002WO-JP006365.

XX 25-JUN-2001; 2001JP-00191837.

XX (TOKE) TOSHIBA KK.

XX Takahashi K, Mishiro S, Oota Y, Hashimoto M, Maekubo H;

XX WPI; 2003-239144/23.

XX P-PSDB; ADE06657.

PT Polynucleotide probes and primers originating in Japanese hepatitis E

PT virus, applicable in chips and kits for detecting hepatitis E virus and

PT its infection.

XX Disclosure; SEQ ID NO 1; 238pp; Japanese.

XX The invention relates to novel polynucleotide probes for detecting
CC hepatitis E virus polynucleotides which contain a sequence of at least 8
CC consecutive nucleotides of the hepatitis E virus genome. The hepatitis E
CC virus genomic sequences are derived from various strains of the Japanese
CC Hepatitis E virus. The probes and primers are applicable in chips and
CC kits for detecting hepatitis E virus and its infection. This sequence
CC represents the open reading frame 1 from the Hepatitis E virus strain
CC JRAL.

SQ Sequence 5138 BP; 966 A; 1470 C; 1380 G; 1322 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.59e+03 Length: 5138
Score: 41.00 Matches: 8
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 53.33% Mismatches: 4
Query Match: 55.41% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x ADE06707 (1-5138)

Qy 1 PheAlaValGluuAsnProMetAsnArgLeuValAlaGluThrLeu 15

Db 248 TTCATTGTGTATAACCCCTCTGAATAGTAGTGGTTCCAAAGCACCTC 204

RESULT 33
 ABL30196
 ID ABL30196 standard; DNA; 6496 BP.
 XX
 AC ABL30196;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42061.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PP 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 42061; 2ipp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 6496 BP; 1733 A; 1444 C; 1490 G; 1829 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.12e+03 Length: 6496
 Score: 41.00 Matches: 9
 Percent Similarity: 64.29% Conservative: 0
 Best Local Similarity: 64.29% Mismatches: 5
 Query Match: 55.41% Indels: 0
 DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x ABL30196 (1-6496)
 QY 2 AlavalGluAenProMetAenArgLeuValAlaGluThrLeu 15
 DB 65 GCTGTGAGAAATCCCGACCGACCTCCTGTGTGAAACACTT 106

RESULT 34
 ADE06697/c
 ID ADE06697 standard; DNA; 7230 BP.
 XX
 AC ADE06697;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Hepatitis E virus strain JRAL genomic sequence.
 XX

Alignment Scores:
 Pred. No.: 2.42e+03 Length: 7230
 Score: 41.00 Matches: 8
 Percent Similarity: 73.33% Conservative: 3
 Best Local Similarity: 53.33% Mismatches: 4
 Query Match: 55.41% Indels: 0
 DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x ADE06697 (1-7230)
 QY 1 PheAlaValGluAenProMetAenArgLeuValAlaGluThrLeu 15
 DB 248 TTCATTGTGTATACCCCTCTGAATAGGATGGTTCCAAAGCACCTC 204

RESULT 35
 ADE06694/c
 ID ADE06694 standard; DNA; 7233 BP.
 XX
 AC ADE06694;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Hepatitis E virus strain JMY-Haw genomic sequence.
 XX
 KW Hepatitis E virus; chips; kit; detection; ds.
 XX
 OS Hepatitis E virus; strain JMY-Haw.
 XX
 PN WO2003000887-A1.
 XX
 PD 03-JAN-2003.
 XX
 PP 25-JUN-2002; 2002WO-JP006365.
 XX
 PR 25-JUN-2001; 2001JP-00191837.
 XX
 PA (TOKE) TOSHIBA KK.
 XX
 PI Takahashi K, Mishihiro S, Oota Y, Hashimoto M, Maekubo H;

KW hepatitis E virus; chips; kit; detection; ds.
 XX
 OS Hepatitis E virus; strain JRAL.
 XX
 PN WO2003000887-A1.
 XX
 PD 03-JAN-2003.
 XX
 PP 25-JUN-2002; 2002WO-JP006365.
 XX
 PR 25-JUN-2001; 2001JP-00191837.
 XX
 PA (TOKE) TOSHIBA KK.
 XX
 PI Takahashi K, Mishihiro S, Oota Y, Hashimoto M, Maekubo H;
 XX
 DR WPI; 2003-239144/23.
 XX
 PT Polynucleotide probes and primers originating in Japanese hepatitis E
 PT virus, applicable in chips and kits for detecting hepatitis E virus and
 PT its infection.
 XX
 PS Claim 1; SEQ ID NO 48; 238pp; Japanese.
 XX
 CC The invention relates to novel polynucleotide probes for detecting
 CC hepatitis E virus polynucleotides which contain a sequence of at least 8
 CC consecutive nucleotides of the hepatitis E virus genome. The hepatitis E
 CC virus genomic sequences are derived from various strains of the Japanese
 CC Hepatitis E virus. The probes and primers are applicable in chips and
 CC kits for detecting hepatitis E virus and its infection. This sequence
 CC represents the genomic sequence from the Hepatitis E virus strain JRAL.
 XX
 SQ Sequence 7230 BP; 1344 A; 2120 C; 1886 G; 1886 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.42e+03 Length: 7230
 Score: 41.00 Matches: 8
 Percent Similarity: 73.33% Conservative: 3
 Best Local Similarity: 53.33% Mismatches: 4
 Query Match: 55.41% Indels: 0
 DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x ADE06697 (1-7230)
 QY 1 PheAlaValGluAenProMetAenArgLeuValAlaGluThrLeu 15
 DB 248 TTCATTGTGTATACCCCTCTGAATAGGATGGTTCCAAAGCACCTC 204

RESULT 35
 ADE06694/c
 ID ADE06694 standard; DNA; 7233 BP.
 XX
 AC ADE06694;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Hepatitis E virus strain JMY-Haw genomic sequence.
 XX
 KW Hepatitis E virus; chips; kit; detection; ds.
 XX
 OS Hepatitis E virus; strain JMY-Haw.
 XX
 PN WO2003000887-A1.
 XX
 PD 03-JAN-2003.
 XX
 PP 25-JUN-2002; 2002WO-JP006365.
 XX
 PR 25-JUN-2001; 2001JP-00191837.
 XX
 PA (TOKE) TOSHIBA KK.
 XX
 PI Takahashi K, Mishihiro S, Oota Y, Hashimoto M, Maekubo H;

```
XX WPI; 2003-239144/23.
XX Polynucleotide probes and primers originating in Japanese hepatitis E
XX virus, applicable in chips and kits for detecting hepatitis E virus and
XX its infection.
XX Claim 1; SEQ ID NO 45; 238pp; Japanese.
XX The invention relates to novel polynucleotide probes for detecting
XX hepatitis E virus polynucleotides which contain a sequence of at least 8
XX consecutive nucleotides of the hepatitis E virus genome. The hepatitis E
XX virus genomic sequences are derived from various strains of the Japanese
XX Hepatitis E virus. The probes and primers are applicable in chips and
XX kits for detecting hepatitis E virus and its infection. This sequence
XX represents the genomic sequence from the Hepatitis E virus strain JMY-
XX Haw.
XX Sequence 7233 BP; 1313 A; 2103 C; 1901 G; 1916 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2.42e+03 Length: 7233
XX Score: 41.00 Matches: 7
XX Percent Similarity: 73.33% Conservative: 4
XX Best Local Similarity: 46.67% Mismatches: 4
XX Query Match: 55.41% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-787-382-20 (1-15) x ADE06694 (1-7233)
XX
XX QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
XX
XX Db 224 TTCATTATGATACCCGCTGATAGGATGATTCAGAGCACCTC 180
XX
XX RESULT 36
XX ID ADV41357/c
XX AC ADV41357 standard; cDNA; 10708 BP.
XX
XX AC ADV41357;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Rat cardiotoxicity marker gene, SEQ ID NO:2223.
XX
XX KW Toxicology screening; drug screening; cardiotoxicity, drug-induced;
XX expression profile; gene expression; myocarditis; heart arrhythmia;
XX tachycardia; myocardial ischemia; angina; hypertension; hypotension;
XX dyspnea; cardiogenic shock; cardiovascular disease; gene; ss.
XX
XX OS Rattus norvegicus.
XX
XX PN WO2004063334-A2.
XX
XX PD 29-JUL-2004.
XX
XX PF 08-JAN-2004; 2004WO-US000240.
XX
XX PR 08-JAN-2003; 2003US-00338044.
XX
XX PA (GENE-) GENE LOGIC INC.
XX
XX PI Mendrick DL, Porter MW, Johnson KR, Higgs B, Castle A;
XX Elashoff M;
XX
XX WPI; 2004-561893/54.
XX DR REFSEQ; NM_031046.
XX
XX PT Predicting a toxic effect of a compound by obtaining a gene expression
XX profile of a tissue or cell sample exposed to the compound and comparing
XX the gene expression profile to a database comprising all of the data
XX given in the specification.
XX
XX Example 1; SEQ ID NO 2223; 520pp; English.
```

```
XX The invention relates to a method of predicting at least one toxic effect
XX of a compound by obtaining a gene expression profile of a tissue or cell
XX sample exposed to the compound and comparing the gene expression profile
XX to a database of toxicity prediction genes which are differentially
XX expressed on exposure to known toxins. The tissue or cell sample is
XX preferably derived from heart tissue, and the predicted toxic effect is
XX especially a cardiotoxic effect such as myocarditis, arrhythmias,
XX tachycardia, myocardial ischemia, angina, hypertension, hypotension,
XX dyspnea, cardiogenic shock or other specific heart pathologies. The
XX invention is based on the elucidation of global changes in gene
XX expression in tissues or cells exposed to known toxins, particularly
XX cardiotoxins, and the identification of individual genes (toxicity
XX markers) that are differentially expressed on toxin exposure. The
XX invention also relates to methods for predicting the progression of a
XX compound's toxic effects, for predicting the cardiotoxicity of a
XX compound, for identifying an agent that modulates the onset or
XX progression of a toxic response, and for predicting which cellular
XX pathways a particular compound will modulate. The invention further
XX relates to sets of at least two hybridization probes specific for
XX toxicity prediction genes, and solid supports and kits comprising them.
XX The method of the invention is useful in toxicology screening for
XX predicting the toxic effects (especially cardiotoxic effects) of
XX compounds such as pharmaceutical agents or environmental pollutants.
XX Sequences ADV9135-ADV41830 represent cardiotoxicity marker
XX polynucleotides of rat origin whose expression is altered on exposure to
XX at least one cardiotoxin. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 10708 BP; 2918 A; 2618 C; 2797 G; 2375 T; 0 U; 0 Other;
```

```
XX Alignment Scores:
XX Pred. No.: 3.92e+03 Length: 10708
XX Score: 41.00 Matches: 10
XX Percent Similarity: 78.57% Conservative: 1
XX Best Local Similarity: 71.43% Mismatches: 3
XX Query Match: 55.41% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-787-382-20 (1-15) x ADV41357 (1-10708)
XX
XX QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
XX
XX Db 9621 GCTGTAAACAACCCCATGTGGCCCTTGCTGGCTGAGAGTTTA 9580
XX
XX RESULT 37
XX ACF67367_07
XX Continuation (8 of 57) of ACF67367 from base 700001 (Photorhabdus luminescens nucleotide
XX WP Sequence split into 57 fragments LOCUS ACF67367 Accession ACF67367
XX WP Fragment Name Begin End
XX WP ACF67367_00 1 110000
XX WP ACF67367_01 100001 210000
XX WP ACF67367_02 200001 310000
XX WP ACF67367_03 300001 410000
XX WP ACF67367_04 400001 510000
XX WP ACF67367_05 500001 610000
XX WP ACF67367_06 600001 710000
XX WP ACF67367_07 700001 810000
XX WP ACF67367_08 800001 910000
XX WP ACF67367_09 900001 1010000
XX WP ACF67367_10 1000001 1110000
XX WP ACF67367_11 1100001 1210000
XX WP ACF67367_12 1200001 1310000
XX WP ACF67367_13 1300001 1410000
XX WP ACF67367_14 1400001 1510000
XX WP ACF67367_15 1500001 1610000
XX WP ACF67367_16 1600001 1710000
XX WP ACF67367_17 1700001 1810000
XX WP ACF67367_18 1800001 1910000
XX WP ACF67367_19 1900001 2010000
XX WP ACF67367_20 2000001 2110000
XX WP ACF67367_21 2100001 2210000
```


CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 480 BP; 176 A; 84 C; 93 G; 127 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 137 Length: 480
Score: 40.00 Matches: 8
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 53.33% Mismatches: 4
Query Match: 54.05% Indels: 0
DB: 8 Gaps: 0

US-10-787-382-20 (1-15) x ACA43050 (1-480)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
DB 299 TTTCGGGTCTCACACCAATATCTTTGTTGTTGAAACGCTG 255

RESULT 43

ABA31096

ID ABA31096 standard; DNA; 567 BP.

XX AC ABA31096;

XX DT 23-JAN-2002 (first entry)

XX DE Probe #9562 for gene expression analysis in human heart cell sample.

XX KW Human; gene expression; heart; microarray; vascular system; probe;

XX KW cardiovascular disease; hypertension; cardiac arrhythmia;

XX KW congenital heart disease; ss.

XX OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US0000666.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WI MPI; 2001-488899/53.

XX PT Single exon nucleic acid probes for analyzing gene expression in human hearts.

XX Claim 1; SEQ ID NO 9562; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 567 BP; 138 A; 101 C; 157 G; 164 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.: 169 Length: 567
Score: 40.00 Matches: 8
Percent Similarity: 73.33% Conservative: 3
Best Local Similarity: 53.33% Mismatches: 4
Query Match: 54.05% Indels: 0
DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x ABA31096 (1-567)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15

DB 48 TTCCATGTGGAAAGACCTTTGCTAGGGTTGTTCACAGGAACTT 92

RESULT 44

ACH72974

ID ACH72974 standard; DNA; 569 BP.

XX AC ACH72974;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #6169.

XX KW Human; probe; ss; gene expression; single exon probe; microarray;

XX KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX PA (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX PI Penn SG, Rank DR, Hanzel DK;

XX WI MPI; 2004-119264/12.

XX PT New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 15; SEQ ID NO 6169; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 569 BP; 161 A; 120 C; 110 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 169 Length: 569
Score: 40.00 Matches: 7
Percent Similarity: 64.29% Conservative: 2
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.05% Indels: 0
DB: 12 Gaps: 0

US-10-787-382-20 (1-15) x ACH72974 (1-569)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
Db 494 TATGCTGTGTCAGTATACCCACAGAGGAGGATTTCTGTGAAC 535

RESULT 45
AAS73628/c
ID AAS73628 standard; cDNA; 913 BP.
XX
AC AAS73628;
XX

13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #9432.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX

PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG09441.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 9432; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 913 BP; 276 A; 218 C; 225 G; 194 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 303 Length: 913
Score: 40.00 Matches: 8
Percent Similarity: 69.23% Conservative: 1
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 54.05% Indels: 0
DB: 5 Gaps: 0

US-10-787-382-20 (1-15) x AAS73628 (1-913)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
Db 457 TTTCGCTAGAAAAGCCCTTTTCAGAGGTTGTGAGGAA 419

RESULT 46
ADN12289/c
ID ADN12289 standard; cDNA; 2310 BP.
XX
AC ADN12289;
XX

01-JUL-2004 (first entry)
XX
DE Nematode iASP polypeptide encoding cDNA.
XX
KW ASPP; iASP; inhibitory ASPP; apoptosis; tumour suppressor protein; p53;
KW cytostatic; cancer; nematode; gene; ss.

XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG09442.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 1; SEQ ID NO 9433; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 2520 BP; 714 A; 636 C; 598 G; 569 T; 0 U; 3 Other;

Alignment Scores:
 Pred. No.: 1.06e+03 Length: 2520
 Score: 40.00 Matches: 8
 Percent Similarity: 69.23% Conservative: 1
 Best Local Similarity: 61.54% Mismatches: 4
 Query Match: 54.05% Indels: 0
 DB: 5 Gaps: 0

US-10-787-382-20 (1-15) x AAS73629 (1-2520)
 QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
 DB 2018 TTTCGCTAGAAAGCCTTTCAGAGGTGGTGAGGGAA 1980

RESULT 49
 ADM01809/c
 ID ADM01809 standard; cDNA; 2591 BP.
 XX
 XX AC ADM01809;
 XX
 XX DT 20-MAY-2004 (first entry)
 XX
 XX DE Human cDNA of the invention SEQ ID NO:494.
 XX
 XX KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.
 XX EP1347046-A1.
 XX 24-SEP-2003.
 XX 12-APR-2002; 2002EP-00008400.
 XX 22-MAR-2002; 2002JP-00137785.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;
 XX WPI; 2003-723558/69.
 XX P-PSDB; ADM04252.
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX Claim 1; SEQ ID NO 494; 305pp; English.
 XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC cDNA sequence of the invention.
 XX SQ Sequence 2591 BP; 744 A; 477 C; 580 G; 790 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.1e+03 Length: 2591
 Score: 40.00 Matches: 7
 Percent Similarity: 83.33% Conservative: 3
 Best Local Similarity: 58.33% Mismatches: 2
 Query Match: 54.05% Indels: 0
 DB: 11 Gaps: 0

US-10-787-382-20 (1-15) x ADM01809 (1-2591)
 QY 4 GluAsnProMetAsnArgLeuValAlaGluThrLeu 15
 DB 1621 GAGAACCCATTAAACAGTCTTATTGCCAACTGCTG 1586

RESULT 50
 ABL14942/c
 ID ABL14942 standard; cDNA; 6692 BP.
 XX
 XX AC ABL14942;
 XX
 XX DT 26-MAR-2002 (first entry)
 XX
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39308.
 XX
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 XX
 XX OS Drosophila melanogaster.
 XX
 XX PN WO200171042-A2.
 XX
 XX PD 27-SEP-2001.
 XX
 XX PF 23-MAR-2001; 2001WO-US009231.

Thu Dec 22 11:37:10 2005

```

XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
XX P-PSDB; ABE70839.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 39308; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABR57737-
CC ABR72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6692 BP; 1978 A; 1255 C; 1270 G; 2189 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 3.53e+03 Length: 6692
Score: 40.00 Matches: 6
Percent Similarity: 83.33% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 54.05% Indels: 0
DB: 4 Gaps: 0
US-10-787-382-20 (1-15) x ABL14942 (1-6692)
QY 3 ValGluAsnProMetAsnArgLeuValAlaGluThr 14
DB 4781 ATCAACACCCATTGATCGATTGTTGTATCTAGACA 4746
Search completed: December 21, 2005, 17:16:44
Job time : 453 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2005, 17:06:14 ; Search time 2610 Seconds
(without alignments)
268.891 Million cell updates/sec

Title: US-10-787-382-20

Perfect score: 74

Sequence: 1 FAVENPMNRLVAETL 15

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5	
Ygapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10787382/runat 16122005 132436 8024/app query fasta_1.199
-DB=EST -QFMT=fasCap -SURFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1:	gb_est1.*
2:	gb_est2.*
3:	gb_est3.*
4:	gb_hic.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_est7.*
9:	gb_gss1.*
10:	gb_gss2.*
11:	gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description

C	1	47	63.5	541	4	CNSOABAJ BX817426 Arabidops
C	2	46	62.2	376	1	AI002749 am98a04.8
C	3	46	62.2	565	7	COL92024 EC32618.5
C	4	46	62.2	874	11	CR821531 GROAA50D
C	5	45	60.8	256	1	AV222732 AV222732
C	6	45	60.8	438	8	DN847029 KECB30-27
C	7	45	60.8	490	7	CN755695 IDOAAA16C

CF587487	USDA-FP 1
CN753056	APHL3LD-X
CN754327	IDOAAA12C
CV834660	IDOACC26B
CV835366	IDOACC28B
CG458219	PUPXV93TB
CA581198	EST0003873
BI084264	602869768
BP886906	BP886906
BM281788	KI20G03.Y
CD830599	BN40.046B
CO675844	DG42-177K
AG132831	Pan trogl
BF731326	603353349
CL670791	PR10163A
CL665378	PR10149C
BF977950	602148422
CL291538	ZMMBB0063
CZ491475	OA_BBA014
CL291538	ZMMBB0063
CB827405	LjNEST74d
DR897668	JGI_XZ742
CE797827	tigr-988-
CC062239	ugma001e0
CZ331571	ZMMBF0039
CA877602	K0958A01-
CC578117	CH240.456
CG841296	Ynhw1910
AZ759493	IM052K03
CF799042	Lr_PAHCF
CG950325	MBEFH66TF
CM171674	104_582.1
CM301651	104_785-1
CM277572	104_751-1
BB303483	BB303483
BB842461	TC3-51G7.
BB845769	TC3-51G7.
CZ422877	1018580.R
BB344850	BB344850
AG170565	Pan trogl
BI912325	603067613
CC339087	OGPBC03TH
CC277571	104_751.1
CC824344	ZMMBB0016
BB924917	odh76G03.
CV266035	WS02028.B
CR839033	GROAAA74B
CL676674	PR10119b
AZ539120	ENTGD12TF-
AV167716	AV167716
AV296711	AV296711
BB465289	BB465289
BB876839	hr33h05.b
BB391641	BB391641
BY649054	BY649054
BQ078906	EST594313
BQ7454136	BJ454136
BF042251	BP250004B
CB436836	684000.MA
CN755347	IDOAAA15C
CB355254	ZF001-P00

C 81	42	56.8	542	3	BM343871	BM343871	rr4a01.y	C 154	41	55.4	560	11	CR244142	CR244142	Forward 8
C 82	42	56.8	579	3	BM092316	BM092916	sa02f09.	C 155	41	55.4	566	9	BH786250	BH786250	fzm0014f0
C 83	42	56.8	594	3	BM343994	BM343994	rr45d11.y	C 156	41	55.4	568	7	CO102578	CO102578	GR_EB003
C 84	42	56.8	608	10	CW513785	CW513785	115.5.105	C 157	41	55.4	569	9	A2300131	A2300131	RPCI-23-1
C 85	42	56.8	622	10	CE738182	CE738182	tigr-g8s-	C 158	41	55.4	573	2	BG520968	BG520968	p803b05.y
C 86	42	56.8	626	10	CE812711	CE812711	tigr-g8s-	C 159	41	55.4	579	9	CC474029	CC474029	CH240_298
C 87	42	56.8	631	1	AW255594	AW255594	ML638 pep	C 160	41	55.4	580	9	CC669780	CC669780	QGV8M48TV
C 88	42	56.8	644	5	BX466398	BX466398		C 161	41	55.4	581	1	A1542067	A1542067	SD08134.5
C 89	42	56.8	655	3	BJ277729	BJ277729		C 162	41	55.4	585	10	CW166348	CW166348	104_575.1
C 90	42	56.8	659	9	BH844795	BH844795	TC3-51M10	C 163	41	55.4	586	10	CG845893	CG845893	OGAC62TV
C 91	42	56.8	664	9	AQ413187	AQ413187	RPCI-11-1	C 164	41	55.4	597	7	CO963847	CO963847	BeE30N10A
C 92	42	56.8	665	6	CA138015	CA138015	SCEPRT204	C 165	41	55.4	596	7	CO966550	CO966550	BeE60N18F
C 93	42	56.8	675	9	CC962185	CC962185	NDL-11401	C 166	41	55.4	600	3	BI632767	BI632767	SD26634.5
C 94	42	56.8	701	9	AQ422337	AQ422337	RPCI-11-1	C 167	41	55.4	602	6	CR538947	CR538947	777044_MA
C 95	42	56.8	719	10	CW570808	CW570808	OA_ABA009	C 168	41	55.4	603	10	CW325753	CW325753	104_820.1
C 96	42	56.8	732	11	CR485728	CR485728	mtA2-154F	C 169	41	55.4	609	8	DR115048	DR115048	1432635_M
C 97	42	56.8	736	6	CB166635	CB166635	IBE603020	C 170	41	55.4	615	3	BI579387	BI579387	RE73412.5
C 98	42	56.8	748	9	CG925243	CG925243	t082m04ba	C 171	41	55.4	622	11	CR867190	CR867190	Sus scrof
C 99	42	56.8	767	9	BZ507891	BZ507891	BONQA05TR	C 172	41	55.4	623	5	BU459724	BU459724	603777648
C 100	42	56.8	769	9	BZ389085	BZ389085	EINCW37TF	C 173	41	55.4	625	5	BQ913305	BQ913305	OHA6P07.y
C 101	42	56.8	778	7	CR528132	CR528132	CR528132	C 174	41	55.4	625	9	BZ866700	BZ866700	CH240_224
C 102	42	56.8	778	10	CW960333	CW960333	AIAX-aab0	C 175	41	55.4	639	8	CV932315	CV932315	FWPcm_17
C 103	42	56.8	793	2	BG822958	BG822958	602727966	C 176	41	55.4	643	9	AQ319700	AQ319700	RPCI11-10
C 104	42	56.8	803	9	CC478198	CC478198	CH240_304	C 177	41	55.4	643	10	CL409977	CL409977	RPCI44_41
C 105	42	56.8	810	7	CN056876	CN056876	Salamande	C 178	41	55.4	648	10	CG073615	CG073615	PUMH78TD
C 106	42	56.8	817	10	CZ242866	CZ242866	AIAX-ae0	C 179	41	55.4	650	9	CC477657	CC477657	CH240_303
C 107	42	56.8	818	10	CZ301608	CZ301608	ZMMB0077	C 180	41	55.4	651	6	CB085251	CB085251	qp82a08.9
C 108	42	56.8	819	10	CG864475	CG864475	ZMMB0027	C 181	41	55.4	658	9	BZ328985	BZ328985	1d74d03.g
C 109	42	56.8	822	10	CZ242489	CZ242489	AIAX-aag3	C 182	41	55.4	659	2	BG302136	BG302136	p803b05.y
C 110	42	56.8	823	6	CD075024	CD075024	MA3-0001U	C 183	41	55.4	659	7	CN768041	CN768041	taf66b11.
C 111	42	56.8	867	9	CC404654	CC404654	PUHUK33TB	C 184	41	55.4	659	10	CW325754	CW325754	104_820.1
C 112	42	56.8	870	7	CO880994	CO880994	BovGen_09	C 185	41	55.4	663	7	CK756213	CK756213	ltu01-2ms
C 113	42	56.8	870	10	AG839415	AG839415	Oryza sat	C 186	41	55.4	663	8	DT001550	DT001550	Mdf8000SM
C 114	42	56.8	911	9	CC100748	CC100748	CSU-K34.1	C 187	41	55.4	663	9	BH734456	BH734456	Mdf8000SM
C 115	42	56.8	953	10	CZ926715	CZ926715	109844825	C 188	41	55.4	667	3	BI579662	BI579662	RE73729.5
C 116	42	56.8	1012	6	CA453826	CA453826	AGENCOURT	C 189	41	55.4	673	6	CF440761	CF440761	EST677106
C 117	42	56.8	1051	10	CN80051B	AL056602	Drosophila	C 190	41	55.4	674	10	CL636131	CL636131	CH243-112
C 118	42	56.8	1101	10	CN8000ZT	AL054596	Drosophila	C 191	41	55.4	675	2	BI171244	BI171244	RE12967.5
C 119	41	55.4	181	2	BA400648	BA400648	BH400648	C 192	41	55.4	676	9	BZ872752	BZ872752	CH240_238
C 120	41	55.4	197	9	BZ890151	BZ890151	CH240_221	C 193	41	55.4	680	9	CC712624	CC712624	OGV8046TV
C 121	41	55.4	225	9	CC491280	CC491280	CH240_334	C 194	41	55.4	684	5	BW272554	BW272554	BW272554
C 122	41	55.4	228	1	AV557572	AV557572	AV557572	C 195	41	55.4	686	11	CR832029	CR832029	GROAAA65A
C 123	41	55.4	256	2	BZ020682	BZ020682	BZ020682	C 196	41	55.4	687	9	BZ048323	BZ048323	1k160b10.
C 124	41	55.4	275	3	BI641088	BI641088	SD24227.5	C 197	41	55.4	688	9	BH664672	BH664672	BOH7254TR
C 125	41	55.4	287	7	CO975301	CO975301	heg90N14H	C 198	41	55.4	690	11	CR499634	CR499634	mtc12-176F
C 126	41	55.4	294	1	AV160435	AV160435	AV160435	C 199	41	55.4	691	6	CA449441	CA449441	2M0161B04
C 127	41	55.4	316	1	AA429548	AA429548	zw74601.r	C 200	41	55.4	693	9	AZ856893	AZ856893	2M0161B04
C 128	41	55.4	322	9	CC543443	CC543443	CH240_425	C 201	41	55.4	696	6	CD373087	CD373087	UI-R-G00-
C 129	41	55.4	361	2	BG557699	BG557699	EM1_55_P0	C 202	41	55.4	701	10	CL409936	CL409936	RPCI44_41
C 130	41	55.4	395	10	AB082309	AB082309	Drosophila	C 203	41	55.4	706	9	CC625602	CC625602	OGVAF59TH
C 131	41	55.4	401	9	AZ036784	AZ036784	RPCI-23-3	C 204	41	55.4	707	7	CN446983	CN446983	GUO_CDNA
C 132	41	55.4	402	9	AQ445016	AQ445016	GSSTC0656	C 205	41	55.4	713	7	CK474995	CK474995	AGENCOURT
C 133	41	55.4	410	3	BP608397	BP608397	BP608397	C 206	41	55.4	715	9	CC773066	CC773066	CH240_12H
C 134	41	55.4	412	9	AQ774176	AQ774176	HS_2050.B	C 207	41	55.4	715	10	CW588062	CW588062	OA_ABA012
C 135	41	55.4	420	9	AQ445015	AQ445015	GSSTC0646	C 208	41	55.4	717	10	CG833440	CG833440	Ynfw0054
C 136	41	55.4	448	8	W00091	W00091	TGSTRzy5e0	C 209	41	55.4	724	10	CW912431	CW912431	BP2142.15
C 137	41	55.4	454	6	CB077852	CB077852	h160b11.g	C 210	41	55.4	725	5	BW254522	BW254522	RW254522
C 138	41	55.4	467	6	CB1713952	CB1713952	AMGNNUC.N	C 211	41	55.4	730	5	BW399499	BW399499	BW399499
C 139	41	55.4	473	3	BI638685	BI638685	SD21039.5	C 212	41	55.4	730	9	BZ685727	BZ685727	PUBED09TD
C 140	41	55.4	477	3	BP897070	BP897070	BP897070	C 213	41	55.4	731	10	CW109686	CW109686	104_482.1
C 141	41	55.4	477	10	CL897573	CL897573	abg43b10.	C 214	41	55.4	731	7	CK478427	CK478427	AGENCOURT
C 142	41	55.4	482	10	CW891285	CW891285	RPCI42_11	C 215	41	55.4	731	9	CC522869	CC522869	CH240_371
C 143	41	55.4	496	3	BQ253042	BQ253042	seo05d06.	C 216	41	55.4	737	7	CO563972	CO563972	AGENCOURT
C 144	41	55.4	497	9	BZ782426	BZ782426	A2SP2C14	C 217	41	55.4	737	10	BX233294	BX233294	Danilo rer
C 145	41	55.4	501	2	BI236935	BI236935	RE33066.5	C 218	41	55.4	744	9	CC590916	CC590916	CH240_391
C 146	41	55.4	508	7	CN553882	CN553882	tae33g02.	C 219	41	55.4	753	9	CC585705	CC585705	CH240_382
C 147	41	55.4	513	6	CA334553	CA334553	NISC_1e10	C 220	41	55.4	754	9	BH513087	BH513087	BOGN072TR
C 148	41	55.4	519	2	BE600821	BE600821	P11_90_E1	C 221	41	55.4	756	6	CF439368	CF439368	EST675713
C 149	41	55.4	525	8	DR116512	DR116512	1431631.M	C 222	41	55.4	756	6	CF444440	CF444440	CF444440
C 150	41	55.4	530	8	CV960793	CV960793	EST348160	C 223	41	55.4	758	9	CC452725	CC452725	ZMMB8C034
C 151	41	55.4	532	1	AW916752	AW916752	PGT348160	C 224	41	55.4	763	8	CX581776	CX581776	TTE000255
C 152	41	55.4	534	10	CW227782	CW227782	104_667.1	C 225	41	55.4	765	5	BW492323	BW492323	GR07126
C 153	41	55.4	547	7	CN578838	CN578838	Mdfw2038F	C 226	41	55.4	771	11	CR807126	CR807126	GROAAA3BE

227	41	55.4	776	9	CC550205	CH240_434	300	40	54.1	416	3	BM625194
C 228	41	55.4	780	9	BZ215419	CH230-371	301	40	54.1	424	6	CA305742
C 229	41	55.4	781	3	BI646103	603276306	302	40	54.1	425	4	AV796178
C 230	41	55.4	782	6	CF452237	EST688582	C 303	40	54.1	430	5	BY157262
C 231	41	55.4	786	3	BI685511	603308982	C 304	40	54.1	431	8	DN346359
C 232	41	55.4	792	9	BH689999	BOMWR95TF	305	40	54.1	440	8	DN346359
C 233	41	55.4	792	10	CL825062	OR_CBA004	C 306	40	54.1	453	10	CG919710
C 234	41	55.4	794	9	BH702782	BOHYN81TF	307	40	54.1	454	9	CC470378
C 235	41	55.4	806	5	BW142868	BW142868	C 308	40	54.1	458	9	AZ153240
C 236	41	55.4	813	9	CC541824	CH240_422	C 309	40	54.1	463	6	CB018032
C 237	41	55.4	818	8	DR932418	EST112395	C 310	40	54.1	478	3	BM113082
C 238	41	55.4	820	9	BZ740953	CGEDS78TC	C 311	40	54.1	483	1	AL930171
C 239	41	55.4	820	9	BZ740956	CGEDS78TM	C 312	40	54.1	486	1	AW035957
C 240	41	55.4	822	10	BX241445	Danio rer	C 313	40	54.1	496	9	BZ861735
C 241	41	55.4	826	8	CV893384	PA004F10	C 314	40	54.1	503	4	AY441057
C 242	41	55.4	826	9	CA497937	CH240_334	C 315	40	54.1	515	11	CR813199
C 243	41	55.4	830	9	AQ858416	nbe00131	C 316	40	54.1	518	6	CD088748
C 244	41	55.4	830	9	CC581393	CH240_376	C 317	40	54.1	527	6	CB401741
C 245	41	55.4	830	10	CG008083	CG008083	C 318	40	54.1	529	2	BF648588
C 246	41	55.4	844	9	BZ408632	OGAAH38TM	C 319	40	54.1	537	5	BX553026
C 247	41	55.4	850	9	BZ138972	CH230-387	C 320	40	54.1	537	6	CD399561
C 248	41	55.4	871	6	CF446583	EST682928	C 321	40	54.1	541	2	BG387269
C 249	41	55.4	879	8	DN066339	JGI_CABD2	C 322	40	54.1	544	10	CZ290167
C 250	41	55.4	880	7	CO973016	BEGON05E	C 323	40	54.1	551	10	CM306882
C 251	41	55.4	880	10	CG438303	CGVHR30TH	C 324	40	54.1	554	1	AU159805
C 252	41	55.4	882	7	CO974333	CG957540	C 325	40	54.1	554	3	BM891913
C 253	41	55.4	884	10	CG052650	PUPRO76TD	C 326	40	54.1	555	9	CC647255
C 254	41	55.4	885	10	CZ328814	ZMBWF0035	C 327	40	54.1	555	9	CC647261
C 255	41	55.4	892	2	BG830768	602767467	C 328	40	54.1	562	9	AZ030534
C 256	41	55.4	892	9	CG973654	ZUAHC33TH	C 329	40	54.1	570	5	BU720959
C 257	41	55.4	902	7	CO975640	CG975640	C 330	40	54.1	573	2	BF649410
C 258	41	55.4	918	11	CNS06X17	AL419153	C 331	40	54.1	577	10	CM106027
C 259	41	55.4	937	10	CG230500	T3 end of	C 332	40	54.1	577	2	BF647021
C 260	41	55.4	957	10	CL090564	ISB1-17N2	C 333	40	54.1	577	6	CA196584
C 261	41	55.4	969	10	CL047142	CH216-65M	C 334	40	54.1	582	7	CO851815
C 262	41	55.4	978	10	CG417187	ZMBWB0002	C 335	40	54.1	586	5	BY782673
C 263	41	55.4	978	10	CL480496	SAIL_325	C 336	40	54.1	588	11	P957L
C 264	41	55.4	1005	10	CL235468	CL480496	C 337	40	54.1	590	1	AJ758771
C 265	41	55.4	1025	9	CC240632	CH261-120	C 338	40	54.1	590	7	CO834889
C 266	41	55.4	1061	10	CL456598	CL456598	C 339	40	54.1	591	6	CD339355
C 267	41	55.4	1177	9	CC242258	CH261-123	C 340	40	54.1	595	6	CB174129
C 268	41	55.4	1239	5	BU501641	AGENCOURT	C 341	40	54.1	595	7	CO908853
C 269	41	55.4	1242	10	DU021821	DU021821	C 342	40	54.1	606	2	BF647562
C 270	41	55.4	1318	3	BQ233334	AGENCOURT	C 343	40	54.1	609	2	BF649961
C 271	40	54.1	166	2	BB433377	BB433377	C 344	40	54.1	611	11	DE025279
C 272	40	54.1	222	1	BB163045	BB163045	C 345	40	54.1	613	10	CM641416
C 273	40	54.1	240	5	C63262	C63262	C 346	40	54.1	619	10	CM042643
C 274	40	54.1	241	2	BB299854	BB299854	C 347	40	54.1	625	1	AU301922
C 275	40	54.1	246	1	AW264700	AW264700	C 348	40	54.1	629	11	CR484779
C 276	40	54.1	271	10	CG887251	CG887251	C 349	40	54.1	630	10	AG157590
C 277	40	54.1	272	3	BP581431	BP581431	C 350	40	54.1	630	10	AG157590
C 278	40	54.1	282	7	CV285296	tak43e08	C 351	40	54.1	633	2	BG448424
C 279	40	54.1	287	2	BB536900	BB536900	C 352	40	54.1	635	3	BI928201
C 280	40	54.1	291	10	AL766882	AL766882	C 353	40	54.1	638	9	BZ322971
C 281	40	54.1	294	1	BB125246	BB125246	C 354	40	54.1	641	11	DE055488
C 282	40	54.1	295	2	BB306396	BB306396	C 355	40	54.1	651	2	BF648419
C 283	40	54.1	295	11	DE108365	DE108365	C 356	40	54.1	651	7	CVN791572
C 284	40	54.1	301	8	CV937853	PMPCm0_00	C 357	40	54.1	651	7	CV007828
C 285	40	54.1	308	2	BG210196	BG210196	C 358	40	54.1	651	11	DE065354
C 286	40	54.1	309	7	CV285088	tak43e08	C 359	40	54.1	653	3	BJ733355
C 287	40	54.1	315	10	CG881506	CG881506	C 360	40	54.1	654	10	CM434174
C 288	40	54.1	323	2	BB459727	BB459727	C 361	40	54.1	654	10	CM434174
C 289	40	54.1	335	1	AV790772	AV790772	C 362	40	54.1	655	2	BG356833
C 290	40	54.1	342	2	BG187405	BG187405	C 363	40	54.1	655	2	BG356833
C 291	40	54.1	359	1	AI152043	AI152043	C 364	40	54.1	657	11	CR341463
C 292	40	54.1	360	5	C62787	C62787	C 365	40	54.1	659	6	CD074045
C 293	40	54.1	360	8	D35007	D35007	C 366	40	54.1	661	6	CD080884
C 294	40	54.1	360	5	CG5473	CG5473	C 367	40	54.1	663	2	CG594900
C 295	40	54.1	372	5	BH732613	BH732613	C 368	40	54.1	663	9	BZ887487
C 296	40	54.1	372	9	BH732613	BH732613	C 369	40	54.1	665	8	CX531977
C 297	40	54.1	391	8	DR108795	DR108795	C 370	40	54.1	666	9	CC570383
C 298	40	54.1	407	9	AQ882677	HS_5431_B	C 371	40	54.1	668	2	BF646345
C 299	40	54.1	409	9	CC887019	CC887019	C 372	40	54.1	668	10	CM190803

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AV796178	AV796178
BY157262	BY157262
DN346359	LIB3551-0
CG919710	MBRFC48TR
CC470378	CH240_143
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BZ861735	CH240_246
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CR813199	GROAAA37C
CD088748	MC1-0053T
CB401741	OSTF198F2
BF648588	NFO49B08E
BX553026	BX553026
CD399561	Gm_CK2124
BG387269	602456016
CZ290167	CP68d01.F
CM306882	104_792_1
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CC647261	OGUDU43TV
AZ030534	RPCI-23-2
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AJ758771	AJ758771
CO834889	LM_GH5_00
CD339355	STrPu536
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BF649961	NFO8EAO8E
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AG157590	Pan trogl
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BI928201	EST548090
BZ322971	ia72d08.g
DE055488	Oryzias_1
BF648419	NFO47B12E
CVN791572	4126318_B
CV007828	zf101-11m
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CR341463	mtel-73F1
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CD080884	LCA03D12C
CG594900	EST493578
BZ887487	CH240_255
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CC570383	CH240_445
BF646345	NFO68H08E
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373	40	54.1	674	7	CO006720	CO006720 EST795055	C 446	40	54.1	863	10	CZ282271	CZ282271 cp22b01.f
374	40	54.1	675	8	DN544035	DN544035 1392928 M	447	40	54.1	867	10	CG216672	CG216672 CG0BT09TH
375	40	54.1	676	8	DN544035	DN544035 1394464 M	448	40	54.1	870	6	CF694500	CF694500 CCAF052TR
376	40	54.1	677	10	DN545413	DN545413 1394464 M	449	40	54.1	871	9	BZ826510	BZ826510 PUGB505TR
377	40	54.1	678	10	AX1057627	AX1057627 0Y31906.x	C 450	40	54.1	878	11	CR797350	CR797350 GRAA0A15D
378	40	54.1	679	1	AJ779001	AJ779001 AJ779001	C 451	40	54.1	880	6	CB565951	CB565951 AGENCOURT
379	40	54.1	680	8	AX118879	AX118879 JGI_XZG65	C 452	40	54.1	883	9	BZ233810	BZ233810 CH230-427
380	40	54.1	681	10	AX063306	AX063306 104_309.1	C 453	40	54.1	883	10	CG298777	CG298777 GGBM77TH
381	40	54.1	682	10	AX063306	AX063306 104_690.1	C 454	40	54.1	886	9	CG551098	CG551098 CH240_436
382	40	54.1	683	5	BU223390	BU223390 603947711	C 455	40	54.1	890	7	CO930738	CO930738 AGENCOURT
383	40	54.1	684	6	CF685373	CF685373 CCAAW59TR	C 456	40	54.1	892	10	CL075513	CL075513 CH216-136
384	40	54.1	685	7	CO868533	CO868533 Mdbb5012a	C 457	40	54.1	899	8	DR942313	DR942313 EST113385
385	40	54.1	686	11	AV165081	AV165081 AV165081	C 458	40	54.1	901	6	CF686776	CF686776 CCAGP19TF
386	40	54.1	687	7	CO010754	CO010754 EST799089	C 459	40	54.1	924	7	CK294694	CK294694 EST757408
387	40	54.1	688	10	AG186214	AG186214 Pan trogl	C 460	40	54.1	925	9	BZ826507	BZ826507 PUGB505TR
388	40	54.1	689	7	CO006721	CO006721 EST795056	C 461	40	54.1	926	6	CD247523	CD247523 AGENCOURT
389	40	54.1	690	3	BJ495021	BJ495021 BJ495021	C 462	40	54.1	926	11	CNS04T3M	CNS04T3M Tetraodon
390	40	54.1	691	713	CG247065	CG247065 1022768 R	C 463	40	54.1	928	10	CZ963113	CZ963113 161109 To
391	40	54.1	692	10	CG887487	CG887487 ZMBBb035	C 464	40	54.1	929	6	CF694494	CF694494 CCAF052TO
392	40	54.1	693	10	AX171555	AX171555 Danilo rer	C 465	40	54.1	937	7	CK285936	CK285936 EST748658
393	40	54.1	694	9	AZ524701	AZ524701 Z35PDD04	C 466	40	54.1	946	7	CK285936	CK285936 EST748658
394	40	54.1	695	5	BY711650	BY711650 BY711650	C 467	40	54.1	946	10	DU007743	DU007743 304859 To
395	40	54.1	696	7	BH540661	BH540661 BQWH69TF	C 468	40	54.1	947	10	DU008473	DU008473 205882 To
396	40	54.1	697	8	CV898705	CV898705 PB014C5 m	C 469	40	54.1	953	10	CZ320499	CZ320499 ZMBB0022
397	40	54.1	698	6	CF678843	CF678843 CCAF40TR	C 470	40	54.1	960	10	DU024894	DU024894 5164 Toma
398	40	54.1	699	10	AX165720	AX165720 Danilo rer	C 471	40	54.1	966	10	CG328691	CG328691 OGXCN71TV
399	40	54.1	700	9	BH730576	BH730576 BOMB711TR	C 472	40	54.1	974	9	CC233849	CC233849 CH261-66D
400	40	54.1	701	8	DR912427	DR912427 EST110396	C 473	40	54.1	978	6	CF695020	CF695020 CCAF052TO
401	40	54.1	702	9	BZ672171	BZ672171 PUBB711TD	C 474	40	54.1	979	5	BU507239	BU507239 AGENCOURT
402	40	54.1	703	10	CG905329	CG905329 RPC142.14	C 475	40	54.1	982	2	BG024012	BG024012 602303226
403	40	54.1	704	8	DN096851	DN096851 JGI_CABE7	C 476	40	54.1	1008	11	CNS05DK6	CNS05DK6 Tetraodon
404	40	54.1	705	7	CO010755	CO010755 EST799090	C 477	40	54.1	1009	9	CC240484	CC240484 CH261-132
405	40	54.1	706	9	BZ316462	BZ316462 1872808.D	C 478	40	54.1	1029	10	CL023150	CL023150 CH216-281
406	40	54.1	707	6	CF695024	CF695024 CCAF054TR	C 479	40	54.1	1043	10	CL037439	CL037439 CH216-43E
407	40	54.1	708	3	BI824316	BI824316 603040733	C 480	40	54.1	1046	10	CNS01528	CNS01528 ZMBBHG000
408	40	54.1	709	10	CL864594	CL864594 TM1-GSS00	C 481	40	54.1	1101	10	CNS00DV5	CL076272 Drosophila
409	40	54.1	710	6	CD079787	CD079787 MA3-99990	C 482	40	54.1	1116	9	CC192052	CC192052 CH261-6M2
410	40	54.1	711	6	CF704703	CF704703 CCAF40TR	C 483	40	54.1	1126	8	DR133510	DR133510 47513731
411	40	54.1	712	10	AG463491	AG463491 Mus muscu	C 484	40	54.1	1166	8	CC194132	CC194132 CH261-560
412	40	54.1	713	1	AL119229	AL119229 DKF2P761C	C 485	40	54.1	1199	8	DR141660	DR141660 49173772
413	40	54.1	714	8	DR941233	DR941233 EST113277	C 486	40	54.1	1262	3	BI689878	BI689878 603310710
414	40	54.1	715	7	BH341457	BH341457 CH230-89L	C 487	40	54.1	1346	10	CL646332	CL646332 CH213-113
415	40	54.1	716	9	CC494353	CC494353 CH240_329	C 488	40	54.1	1390	8	DN716204	DN716204 CNB111-E0
416	40	54.1	717	6	CF680634	CF680634 CCAF057TF	C 489	40	54.1	1508	3	BM803190	BM803190 AGENCOURT
417	40	54.1	718	1	AJ793883	AJ793883 AJ793883	C 490	40	54.1	1666	8	DN987266	DN987266 MSU_28F_2
418	40	54.1	719	8	AX751615	AX751615 AGENCOURT	C 491	40	54.1	210	1	BB000247	BB000247 BB000247
419	40	54.1	720	11	CR823369	CR823369 GROAA53C	C 492	40	54.1	467	9	AQ680174	AQ680174 HS_5470_A
420	40	54.1	721	10	CM704704	CM704704 AIAA-aab9	C 493	40	54.1	566	9	AZ499990	AZ499990 IM0338B07
421	40	54.1	722	2	BG585003	BG585003 EST486765	C 494	40	54.1	596	5	BU781385	BU781385 kb18f05.Y
422	40	54.1	723	10	CM523052	CM523052 OP_Ba001	C 495	40	54.1	804	8	DR779203	DR779203 BAAC-PNPI
423	40	54.1	724	10	CG3699205	CG3699205 MBECD56TR	C 496	40	54.1	804	8	DR779203	DR779203 BAAC-PNPI
424	40	54.1	725	9	BZ394032	BZ394032 EINBU57TR	C 497	40	54.1	121	9	CC040298	CC040298 3591_I_13
425	40	54.1	726	6	CF695688	CF695688 CCAHCL17TR	C 498	40	54.1	156	1	AW799204	AW799204 RCO-UM005
426	40	54.1	727	5	BQ505997	BQ505997 EST613412	C 499	40	54.1	159	1	AA168211	AA168211 ms51f11.r
427	40	54.1	728	6	CF680650	CF680650 CCAF057TR	C 500	40	54.1	170	1	AA371700	AA371700 EST83571
428	40	54.1	729	8	AX508822	AX508822 JGI_XZG53							
429	40	54.1	730	6	CF676373	CF676373 CCAF40TR							
430	40	54.1	731	10	AX2281891	AX2281891 cp19e03.r							
431	40	54.1	732	9	BH725214	BH725214 BOMBA23TR							
432	40	54.1	733	8	DR500671	DR500671 WS02921.C							
433	40	54.1	734	8	CB635261	CB635261 OSIIE15H							
434	40	54.1	735	6	CB983164	CB983164 AGENCOURT							
435	40	54.1	736	10	DU069910	DU069910 137333 To							
436	40	54.1	737	6	CF695682	CF695682 CCAHCL17TF							
437	40	54.1	738	6	CF686782	CF686782 CAGP19TR							
438	40	54.1	739	8	DR156332	DR156332 EST110717							
439	40	54.1	740	11	CR824747	CR824747 GROAA55C							
440	40	54.1	741	8	CD049473	CD049473 AGENCOURT							
441	40	54.1	742	8	DN981657	DN981657 SV6_39F08							
442	40	54.1	743	10	CG328888	CG328888 OG0BN77TH							
443	40	54.1	744	10	AG886962	AG886962 Oryza sat							
444	40	54.1	745	8	AX391333	AX391333 JGI_XZT38							
445	40	54.1	746	8	DN981658	DN981658 SV6_39F09							

ALIGNMENTS

RESULT 1	541 bp	mrna	linear	HTC	06-FEB-2004
LOCUS	CNSOABAJ	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTSL12F12 of Silique of strain col-0 of Arabidopsis thaliana (thale cress)			
DEFINITION	CNSOABAJ/c				
ACCESSION	BX817426				
VERSION	BX817426.1	GI:42471008			
KEYWORDS	HTC; GSIT cDNA				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	rosids; eurosids II; Brassicales; Arabidopsi.				

REFERENCE 1 (bases 1 to 541)
 AUTHORS Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
 TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out full-length libraries construction in Temple G.
 Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.
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 source
 Location/Qualifiers
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 /db_xref="taxon:3702"
 /clone="GSLTSL1212F12"
 /tissue_type="Silique"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Alignment Scores:
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 Score: 47.00 Matches: 9
 Percent Similarity: 90.00% Conservative: 0
 Best Local Similarity: 90.00% Mismatches: 1
 Query Match: 63.51% Indels: 0
 DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x CNS0ABAJ (1-541)
 QY 5 AnProMetAsnArgLeuValAlaGluThr 14
 DB 489 AATCCATGACAGATTGGCAGCGAGACC 460
 RESULT 2
 AI002749/c
 LOCUS am98a04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
 DEFINITION IMAGE:1684110 3', similar to TR:Q13500 Q13500 DYSTROBREVIN-EPSILON.
 ; mRNA sequence.
 ACCESSION AI002749
 VERSION AI002749.1 GI:3203163
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 376)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WASHU-NCI human EST Project
 Unpublished (1997)

REFERENCE 1 (bases 1 to 541)
 AUTHORS Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
 TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out full-length libraries construction in Temple G.
 Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.
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 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSLTSL1212F12"
 /tissue_type="Silique"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Alignment Scores:
 Pred. No.: 65.4 Length: 541
 Score: 47.00 Matches: 9
 Percent Similarity: 90.00% Conservative: 0
 Best Local Similarity: 90.00% Mismatches: 1
 Query Match: 63.51% Indels: 0
 DB: 4 Gaps: 0

US-10-787-382-20 (1-15) x CNS0ABAJ (1-541)
 QY 5 AnProMetAsnArgLeuValAlaGluThr 14
 DB 489 AATCCATGACAGATTGGCAGCGAGACC 460
 RESULT 2
 AI002749/c
 LOCUS am98a04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
 DEFINITION IMAGE:1684110 3', similar to TR:Q13500 Q13500 DYSTROBREVIN-EPSILON.
 ; mRNA sequence.
 ACCESSION AI002749
 VERSION AI002749.1 GI:3203163
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 376)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WASHU-NCI human EST Project
 Unpublished (1997)

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..376
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1684110"
 /sex="male"
 /tissue_type="schizophrenic brain S-11 frontal lobe"
 /dev_stage="34 years old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene schizo brain S11"
 /note="Vector: Bluescript SK-; Site_1: EcoRI; Library constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Random primed into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Material obtained by Johnston N., Torrey, E.F., Yolken R., and the Stanley Neuropathology Consortium - Analysis of RNAs from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurology Laboratory, Johns Hopkins School of Medicine, Baltimore MD."

ORIGIN
 Alignment Scores:
 Pred. No.: 68.6 Length: 376
 Score: 46.00 Matches: 9
 Percent Similarity: 76.92% Conservative: 1
 Best Local Similarity: 69.23% Mismatches: 3
 Query Match: 62.16% Indels: 0
 DB: 1 Gaps: 0

US-10-787-382-20 (1-15) x AI002749 (1-376)
 QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
 DB 272 TTTCGCTAGAAACCCCTTTTCAGAGGTGGTGGAGGAA 234
 RESULT 3
 CO192024
 LOCUS EC32618.5prime Exelixis FlyTag ML01 pSPORT-Tag21 Drosophila
 DEFINITION melanogaster cDNA clone EC32618 5, mRNA sequence.
 ACCESSION CO192024
 VERSION CO192024.1 GI:49003199
 KEYWORDS EST.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS Chen, F., Lagueux, M., Cheung, L.M., Chong, A., Goldschmidt, S., Hubsan, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C., Orton, A., Shao, A., Platt, D., and Swimmer, C.
 EXELIXIS FlyTag EST Project ML01 Library
 Unpublished (2004)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA


```

Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EC326 row: B column: 6
High quality sequence stop: 504.
Location/Qualifiers
1. .565
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EC32618"
/dev_stage="3rd instar larva"
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NotI; Site 2: XhoI; RNA was isolated from fat body from
3rd instar larva challenged with gram-/ bacteria. cDNA
was oligodT primed."

ORIGIN
Alignment Scores:
Pred. No.: 109 Length: 565
Score: 46.00 Matches: 8
Percent Similarity: 83.33% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 2
Query Match: 62.16% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CO192024 (1-565)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAla 12
||||| :|||:|||||:|||||
Db 177 TTTGCTGCTGCAACCCATTAAACCGATTGATCGCG 212

RESULT 4
CR821531
LOCUS
DEFINITION
CR821531 874 bp DNA linear GSS 27-SEP-2004
GROAAASODE10FM1 INRA BAC Bos taurus genomic clone INRA8_810F01, DNA
sequence, genomic survey sequence.
ACCESSION
CR821531.1 GI:52757619
VERSION
GSS.
KEYWORDS
Bos taurus (cow)
SOURCE
Bos taurus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 874)
Eggen,A., Schibler,L. and Roy,A.
Bovine BAC End Sequences from the INRA bovine BAC library
Unpublished
2 (bases 1 to 874)
Genoscope.
Direct Submission
Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Contact: Andre Eggen
Department of Animal Genetics - LGBC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 810 row: F column: 01
Seq primer: M13 Forward
Class: BAC ends.
Location/Qualifiers
1. .874
/organism="Bos taurus"

FEATURES
source

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/db_xref="taxon:9913"
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/cell_type="fibroblast"
/clone_lib="INRA bovine BAC"
/note="Vector: pBeloBAC11; Site 1: HindIII; Holstein bull;
INRA Bovine BAC library (Male) produced by Andre Eggen
Genoscope sequence ID : GROAAASODE10FM1"

ORIGIN
Alignment Scores:
Pred. No.: 180 Length: 874
Score: 46.00 Matches: 8
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 62.16% Indels: 0
DB: 11 Gaps: 0

US-10-787-382-20 (1-15) x CR821531 (1-874)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
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Db 722 TTTGCTGCTGGAATCCTATGAACACAGAAATCTGGCAGACT 763

RESULT 5
AV222732/2
LOCUS
DEFINITION
AV222732 256 bp mRNA linear EST 14-NOV-2001
extra embryonic tissue Mus musculus cDNA clone 3830403007 3', mRNA
sequence.
ACCESSION
AV222732
VERSION
AV222732.1 GI:6171909
KEYWORDS
EST.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 256)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tomimaga,N.,
Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitanai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

```



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/clone="ID0AAA16CD02"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

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ORIGIN

Alignment Scores:

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Pred. No.: 148 Length: 490
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservatives: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

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US-10-787-382-20 (1-15) x CN755695 (1-490)

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QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
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Db 45 TTTATCATCGATAACCCACTCAATAGATTATCATAGAA 7

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RESULT 8

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CF587487/c
LOCUS CF587487 504 bp mRNA linear EST 25-SEP-2003
DEFINITION USDA-FP 120800-038 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon
pisum cDNA clone WHAP- 005_E05 5', mRNA sequence.

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ACCESSION CF587487
VERSION CF587487.1 GI:35505710
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)

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ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 504)

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REFERENCE
AUTHORS Hunter,W.B., Dang,P.M., Stern,D. and Lapointe,S.L.
TITLE Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
JOURNAL Unpublished (2004)
COMMENT Contact: Wayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS

```

```

2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ehrl.ars.usda.gov
Seq primer: T3 Primer.

```

FEATURES

source

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1..504
Location/Qualifiers
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP- 005_E05"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="XLI-Blue"

```

```

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Srinii
Kambhampati; Peter Dearn; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Tuner score of 20 or better.

```

Sequencing of clones by Dr. PM Dang, US. Horticultural Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN

Alignment Scores:

```

Pred. No.: 152 Length: 504
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservatives: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 6 Gaps: 0

```

US-10-787-382-20 (1-15) x CF587487 (1-504)

```

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
||||| : : : : : : : : : : : : : : : : : : : :
Db 174 TTTATCATCGATAACCCACTCAATAGATTATCATAGAA 136

```

RESULT 9

```

CN753056/c
LOCUS CN753056 539 bp mRNA linear EST 19-MAY-2004
DEFINITION AphL3LD-XI-F6 AphL3LD Acyrthosiphon pisum cDNA clone AphL3LDXIF6
5', mRNA sequence.

```

```

ACCESSION CN753056
VERSION CN753056.1 GI:47518053
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)

```

```

ORGANISM
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 539)

```

```

REFERENCE
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes

```

```

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.
PCR PRIMERS
FORWARD: GCCGCATACCTTCGTATAGCA
Plate: XI row: F column: 6.

```

FEATURES

source

```

1..539
Location/Qualifiers
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="AphL3LDXIF6"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOPI0"
/clone_lib="AphL3LD"
/note="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI;
Sample name: AphL3LD ; Plant growth place: INRA-Rennes,
UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 18/01/2003 ; Harvesting
date: 03/02/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
long photoperiod (16-hr light/8-hr dark at 18 c)"

```

ORIGIN

Alignment Scores:

```

Pred. No.: 165 Length: 539
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservatives: 5
Best Local Similarity: 46.15% Mismatches: 2

```

Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CN753056 (1-539)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
DB 377 TTTATCATCGATAACCCCACTCAATAGAAATTATCATAGAA 339

RESULT 10
CN754327/c
LOCUS CN754327
DEFINITION ID0AAA12CG12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA12CG12
5', mRNA sequence.

ACCESSION CN754327
VERSION CN754327.1 GI:47519324
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 625)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 12 row: G column: 12.
Location/Qualifiers
1. 625
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA12CG12"
/issue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApKS"
/note="Vector: PBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

ALIGNMENT SCORES
Pred. No.: 195 Length: 625
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CN754327 (1-625)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
DB 377 TTTATCATCGATAACCCCACTCAATAGAAATTATCATAGAA 339

RESULT 10
CN754327/c
LOCUS CN754327
DEFINITION ID0AAA12CG12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA12CG12
5', mRNA sequence.

ACCESSION CN754327
VERSION CN754327.1 GI:47519324
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 625)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 12 row: G column: 12.
Location/Qualifiers
1. 625
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA12CG12"
/issue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApKS"
/note="Vector: PBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

ALIGNMENT SCORES
Pred. No.: 195 Length: 625
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CN754327 (1-625)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
DB 377 TTTATCATCGATAACCCCACTCAATAGAAATTATCATAGAA 339

RESULT 10
CN754327/c
LOCUS CN754327
DEFINITION ID0AAA12CG12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA12CG12
5', mRNA sequence.

ACCESSION CN754327
VERSION CN754327.1 GI:47519324
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 625)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 12 row: G column: 12.
Location/Qualifiers
1. 625
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA12CG12"
/issue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApKS"
/note="Vector: PBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

ALIGNMENT SCORES
Pred. No.: 195 Length: 625
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CN754327 (1-625)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
DB 377 TTTATCATCGATAACCCCACTCAATAGAAATTATCATAGAA 339

RESULT 10
CN754327/c
LOCUS CN754327
DEFINITION ID0AAA12CG12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA12CG12
5', mRNA sequence.

ACCESSION CN754327
VERSION CN754327.1 GI:47519324
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 625)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 12 row: G column: 12.
Location/Qualifiers
1. 625
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA12CG12"
/issue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
/clone_lib="ApKS"
/note="Vector: PBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA ; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University ; Soil conditions: Soil ; Sowing date: 01/06/1999 ; Harvesting date: 01/06/1999 ; Stress date: no stress ; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

ALIGNMENT SCORES
Pred. No.: 195 Length: 625
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x CN754327 (1-625)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
DB 377 TTTATCATCGATAACCCCACTCAATAGAAATTATCATAGAA 339

RESULT 10
CN754327/c
LOCUS CN754327
DEFINITION ID0AAA12CG12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AAA12CG12
5', mRNA sequence.

ACCESSION CN754327
VERSION CN754327.1 GI:47519324
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 625)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endos

```

VERSION CV835366.1 GI:55801049
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 902)
AUTHORS Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
TITLE Annotated ESTs of the pea aphid
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 28B row: A column: 10.
FEATURES
source
1..902
Location/Qualifiers
/organism="Acyrthosiphon pisum"
/mol_type="rRNA"
/cultivar="P123"
/db_xref="taxon:7029"
/clone="IDOACC28BA10"
/tissue_type="head"
/dev_stage="larvae L3 (parthenogenetic females)"
/lab_host="Xl1-Blue"
/clone_lib="IDOACC"
/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDOACC ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting
date: 17/10/2003 ; Description: aphids inoculated on
one-week old Vicia faba germinations under non sterile
conditions experimental condition: long photoperiod (16-hr
light/8-hr dark at 18 degC)"

ORIGIN
Alignment Scores:
Pred. No.: 297 Length: 902
Score: 45.00 Matches: 6
Percent Similarity: 84.62% Conservative: 5
Best Local Similarity: 46.15% Mismatches: 2
Query Match: 60.81% Indels: 0
DB: 8 Gaps: 0

US-10-787-382-20 (1-15) x CV835366 (1-902)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
|||||:|||||:|||||:|||||:|||||:|||||
Db 534 TTATCATCGATACCCACTCAATAGATATCATAGAA 496

RESULT 13
CG458219/c 959 bp DNA linear GSS 17-SBP-2003
LOCUS PUFV93TBC_ZM_0.6.1.0 KB Zea mays genomic clone ZMBT0757P18,
genomic survey sequence.
ACCESSION CG458219
VERSION CG458219.1 GI:34843219
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 959)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFV93TBC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1..959
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBT0757P18"
/clone_lib="ZM 0.6.1.0 KB"
/note="Vector: pCE4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 318 Length: 959
Score: 45.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 60.81% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x CG458219 (1-959)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
|||||:|||||:|||||:|||||:|||||:|||||
Db 592 TTCTCTGTGGAGAACCTTAAAGTCGCTCCGAGAGAGACC 551

RESULT 14
CA584198 1000 bp mRNA linear EST 19-NOV-2002
LOCUS EST003873 Mycelium and yeast cells from Paracoccidioides
brasiliensis Paracoccidioides brasiliensis cDNA, mRNA sequence.
ACCESSION CA584198.1 GI:25132589
VERSION CA584198.1
KEYWORDS EST.
SOURCE Paracoccidioides brasiliensis
ORGANISM Paracoccidioides brasiliensis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.
REFERENCE 1 (bases 1 to 1000)
AUTHORS Felipe,M.S.S., Andrade,R.V., Petrofeza,S.S., Maranhao,A.Q.,
Torres,F.A., Albuquerque,P., Arraes,F.B.M., Arruda,M.,
Azevedo,M.O., Baptista,A.J., Bataus,L.A., Borges,C.L., Campos,E.G.,
Cruz,M.R., Daher,B.S., Dantas,A., Ferreira,M.A.S.V., Ghil,G.V.,
Jesuino,R.S.A., Kyaw,C.M., Leitao,L., Martins,C.R., Moraes,L.M.P.,
Neves,E.O., Nicola,A., Alves,E.S., Parente,J.A., Pereira,M.,
Pocas-Fonseca,M.J., Resende,R., Ribeiro,B.M., Saldanha,R.R.,
Santos,S.C., Silva-Pereira,I., Silva,M.A.S., Silveira,E.,
Simoes,I.C., Soares,R.B.A., Souza,D.P., de-Souza,M.T.,
Andrade,E.V., Xavier,M.A.S., Veiga,H.P., Venancio,E.J.,
Carvalho,M.J.A., Oliveira,A.G., Inoue,M.K., Almeida,N.F.,
Walter,M.E.M.T., Soares,C.M.A. and Brigido,M.M.
Transcriptome characterization of the dimorphic and pathogenic
fungus Paracoccidioides brasiliensis by EST analysis
Yeast 20 (3), 263-271 (2003)
12557278
Contact: Felipe MSS
Laboratory of Molecular Biology
Institute of Biology - University of Brasilia
Campus Universitario, Aea Norte, Brasilia, DF 70910-900, BRA
Tel: 55 61 307 2423
Fax: 55 61 349 8411

```

Email: msueli@unb.br
 Seq primer: T7 Sequencing primer.
 Location/Qualifiers
 1..1000
 /organism="Paracoccidioides brasiliensis"
 /mol_type="rRNA"
 /strain="Pb01"
 /db_xref="taxon:121759"
 /clone_lib="Mycelium and yeast cells from Paracoccidioides brasiliensis"
 /note="Pb Lambda Zap Express Library"

ORIGIN

Alignment Scores:
 Pred. No.: 334 Length: 1000
 Score: 45.00 Matches: 8
 Percent Similarity: 78.57% Conservative: 3
 Best Local Similarity: 57.14% Mismatches: 3
 Query Match: 60.81% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x CA584198 (1-1000)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
 DB 723 TTTGTTGTAGACACCCNATAATAGATTAAACGAAACA 764

RESULT 15
 B1084264
 LOCUS
 DEFINITION
 mRNA sequence. 1012 bp mRNA linear EST 20-JUN-2001
 B1084264
 VERSION
 B1084264.1 GI:14502594

KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 1 (bases 1 to 1012)
 AUTHORS
 NIH-MGC http://mgi.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1821 row: h column: 18
 High quality sequence stop: 1.

FEATURES

source

1..1012
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5014337"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site: 1: XhoI;
 Site: 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene), and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 338 Length: 1012
 Score: 45.00 Matches: 9
 Percent Similarity: 81.82% Conservative: 0
 Best Local Similarity: 81.82% Mismatches: 2
 Query Match: 60.81% Indels: 0
 DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x B1084264 (1-1012)

QY 3 ValGluAsnProMetAsnArgLeuValAlaGlu 13
 DB 859 GTGCGAAACCCGATGATAGACTATGCGCAGAA 891

RESULT 16
 B1084264
 LOCUS
 DEFINITION
 mRNA sequence. 471 bp mRNA linear EST 16-MAR-2005
 B1084264
 VERSION
 B1084264.1 GI:58230377

KEYWORDS
 EST.
 SOURCE
 Lycopersicon esculentum (Solanum lycopersicum)
 ORGANISM
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 471)
 YAMAMOTO, N., TSUGANE, T., WATANABE, M., YANO, K., MAEDA, F., KUWATA, C.,
 MOEZ, T., NISHIMURA, S. and SHIBATA, D.
 Expressed sequence tags from the laboratory-grown tomato
 (Lycopersicon esculentum) cultivar Micro-Tom and mining for single
 nucleotide polymorphisms and insertions/deletions in tomato
 cultivars
 Unpublished (2005)
 CONTACT: Daisuke Shibata
 Kazusa DNA Research Institute;
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3947
 Fax: 81-438-52-3948
 Email: shibata@kazusa.or.jp
 This clone was obtained at our laboratory.
 Please visit our web site
 URL: http://www.kazusa.or.jp/jsol/microtom/indexj.html (in Japanese)
 URL: http://www.kazusa.or.jp/jsol/microtom/indexj.html (in English).

FEATURES
 Location/Qualifiers
 1..471
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Micro-Tom"
 /db_xref="taxon:4081"
 /clone="FA35DB12"
 /tissue_type="maturing fruit"
 /clone_lib="Lycopersicon esculentum maturing fruit"

ORIGIN

Alignment Scores:
 Pred. No.: 224 Length: 471
 Score: 44.00 Matches: 8
 Percent Similarity: 76.92% Conservative: 2
 Best Local Similarity: 61.54% Mismatches: 3
 Query Match: 59.46% Indels: 0
 DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x B1084264 (1-471)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13
 DB 13 TTCTCTGTGTAACCCCACTTAATAGATTGATAAAGAA 51

RESULT 17
 B1084264

Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.

FEATURES

source

```
1. .572
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG42-liver"
/notes="Organ: liver; Vector: Dog pBluescript LION"
```

ORIGIN

Alignment Scores:
Pred. No.: 280 Length: 572
Score: 44.00 Matches: 9
Percent Similarity: 78.57% Conservativeness: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 59.46% Indels: 0
DB: 7 Gaps: 0

US-10-787-382-20 (1-15) x C0675844 (1-572)

QY 2 AlavalGluAenPrometAsnArgLeuValalaGluThrLeu 15
|||||
Db 439 GCTTTGAGAACCCCATCGGAGCTTCGATCCGAAACTCTG 480

RESULT 20

AG132831
LOCUS AG132831 675 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-145F04.F, genomic survey sequence.
ACCESSION AG132831
VERSION AG132831.1 GI:16662509
KEYWORDS GSS.

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB

TITLE

Unpublished

REFERENCE

2 (bases 1 to 675)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

```
1. .675
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-145F04.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
```

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 339 Length: 675
Score: 44.00 Matches: 7
Percent Similarity: 78.57% Conservativeness: 4
Best Local Similarity: 59.00% Mismatches: 3
Query Match: 59.46% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x AG132831 (1-675)

QY 2 AlavalGluAenPrometAsnArgLeuValalaGluThrLeu 15
|||||
Db 381 GCAATTCAGAACCTCAGAACAGAACATCTCAGAACATTCG 422

RESULT 21

BI731326/c

LOCUS BI731326 797 bp mRNA linear EST 20-SEP-2001

DEFINITION 60335349F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5360557 5',
mRNA sequence.

ACCESSION BI731326

VERSION BI731326.1 GI:15708339

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 797)

REFERENCE

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11917 row: b column: 14

High quality sequence stop: 605.

FEATURES

Location/Qualifiers

1. .797

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:5360557"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 409 Length: 797
Score: 44.00 Matches: 8
Percent Similarity: 78.57% Conservativeness: 3
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 59.46% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x BI731326 (1-797)

QY 2 AlavalGluAenPrometAsnArgLeuValalaGluThrLeu 15
|||||
Db 139 GCTGTGAGAACCCCATCTTAGCTGTTGGGAGAACATC 98


```

RESULT 22
CL670791          817 bp      DNA      linear      GSS 09-JUL-2004
LOCUS             PRI0163a.B21 (817) Mixed stage fosmid library of P.
DEFINITION        pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION         CL670791.1 GI:50169091
VERSION           CL670791
KEYWORDS          GSS.
SOURCE            Pristionchus pacificus
ORGANISM          Pristionchus pacificus
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                  Neodiplogasteridae; Pristionchus.
REFERENCE         1 (bases 1 to 817)
AUTHORS           Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE            AppaDB: an AcedB database for the nematode satellite organism
JOURNAL           Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED            14681447
COMMENT           Contact: Sommer RJ
                  Evolutionary Biology
                  Max-Planck-Institute for Developmental Biology
                  Spemannstr. 37-39, Tuebingen D-72076, Germany
                  Tel: 00497071601371
                  Fax: 00497071601498
                  Email: ralf.sommer@tuebingen.mpg.de
                  This library was generated at Caltech, Pasadena, USA and end
                  sequenced at Vancouver, Canada.
                  Seq primer: T7
                  Class: fosmid ends.
FEATURES          Location/Qualifiers
source            1..817
                  /organism="Pristionchus pacificus"
                  /mol_type="genomic DNA"
                  /strain="California"
                  /db_xref="taxon:54126"
                  /clone_lib="Mixed stage fosmid library of P. pacificus
                  var. California"
                  /note="vector: pBpifos-5 Fosmid vector"
ORIGIN
Alignment Scores:
Pred. No.:        421          Length:      817
Score:            44.00        Matches:      8
Percent Similarity: 76.92%     Conservative: 2
Best Local Similarity: 61.54%  Mismatches:    3
Query Match:      59.46%       Indels:       0
DB:               10          Gaps:        0

US-10-787-382-20 (1-15) x CL670791 (1-817)

Qy      2 AlaValGluAsnProMetAsnArgGluValAlaGluThr 14
       |||||  |||||  |||  |||||  |||||  |||||
Db      326 GCGATAAACACCCGCAAAACGCGTCGTCGCTCAAC 364

RESULT 23
CL665378/c
LOCUS             CL665378 (832) Mixed stage fosmid library of P.
DEFINITION        pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION         CL665378.1 GI:50156923
VERSION           CL665378
KEYWORDS          GSS.
SOURCE            Pristionchus pacificus
ORGANISM          Pristionchus pacificus
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                  Neodiplogasteridae; Pristionchus.
REFERENCE         1 (bases 1 to 832)
AUTHORS           Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE            AppaDB: an AcedB database for the nematode satellite organism
JOURNAL           Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED            14681447
COMMENT           Contact: Sommer RJ
                  Evolutionary Biology
                  Max-Planck-Institute for Developmental Biology
                  Spemannstr. 37-39, Tuebingen D-72076, Germany
                  Tel: 00497071601371
                  Fax: 00497071601498
                  Email: ralf.sommer@tuebingen.mpg.de
                  This library was generated at Caltech, Pasadena, USA and end
                  sequenced at Vancouver, Canada.
                  Seq primer: T7
                  Class: fosmid ends.
FEATURES          Location/Qualifiers
source            1..832
                  /organism="Pristionchus pacificus"
                  /mol_type="genomic DNA"
                  /strain="California"
                  /db_xref="taxon:54126"
                  /clone_lib="Mixed stage fosmid library of P. pacificus
                  var. California"
                  /note="vector: pBpifos-5 Fosmid vector"
ORIGIN
Alignment Scores:
Pred. No.:        421          Length:      817
Score:            44.00        Matches:      8
Percent Similarity: 76.92%     Conservative: 2
Best Local Similarity: 61.54%  Mismatches:    3
Query Match:      59.46%       Indels:       0
DB:               10          Gaps:        0

US-10-787-382-20 (1-15) x CL670791 (1-817)

Qy      2 AlaValGluAsnProMetAsnArgGluValAlaGluThr 14
       |||||  |||||  |||  |||||  |||||  |||||
Db      326 GCGATAAACACCCGCAAAACGCGTCGTCGCTCAAC 364

RESULT 23
CL665378/c
LOCUS             CL665378 (832) Mixed stage fosmid library of P.
DEFINITION        pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION         CL665378.1 GI:50156923
VERSION           CL665378
KEYWORDS          GSS.
SOURCE            Pristionchus pacificus
ORGANISM          Pristionchus pacificus
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                  Neodiplogasteridae; Pristionchus.
REFERENCE         1 (bases 1 to 832)
AUTHORS           Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE            AppaDB: an AcedB database for the nematode satellite organism
JOURNAL           Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED            14681447
COMMENT           Contact: Sommer RJ
                  Evolutionary Biology
                  Max-Planck-Institute for Developmental Biology
                  Spemannstr. 37-39, Tuebingen D-72076, Germany
                  Tel: 00497071601371
                  Fax: 00497071601498
                  Email: ralf.sommer@tuebingen.mpg.de
                  This library was generated at Caltech, Pasadena, USA and end
                  sequenced at Vancouver, Canada.
                  Seq primer: T7
                  Class: fosmid ends.
FEATURES          Location/Qualifiers
source            1..832
                  /organism="Pristionchus pacificus"
                  /mol_type="genomic DNA"
                  /strain="California"
                  /db_xref="taxon:54126"
                  /clone_lib="Mixed stage fosmid library of P. pacificus
                  var. California"
                  /note="vector: pBpifos-5 Fosmid vector"
ORIGIN
Alignment Scores:
Pred. No.:        421          Length:      817
Score:            44.00        Matches:      8
Percent Similarity: 76.92%     Conservative: 2
Best Local Similarity: 61.54%  Mismatches:    3
Query Match:      59.46%       Indels:       0
DB:               10          Gaps:        0

US-10-787-382-20 (1-15) x CL670791 (1-817)

Qy      2 AlaValGluAsnProMetAsnArgGluValAlaGluThr 14
       |||||  |||||  |||  |||||  |||||  |||||
Db      326 GCGATAAACACCCGCAAAACGCGTCGTCGCTCAAC 364

```


Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15

High quality sequence stop: 517.

FEATURES
source

```

1. .517
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="ugma001e002a1"
/clone_lib="ugma unfiltered library (libid: 146)"
/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBSK(-) vector
and electroporated into E. coli cells. This is a standard
(unfiltered) whole genome shotgun library."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 397 Length: 517
Score: 43.00 Matches: 9
Percent Similarity: 73.3% Conservative: 2
Best Local Similarity: 60.0% Mismatches: 4
Query Match: 58.11% Indels: 0
DB: 9 Gaps: 0

```

US-10-787-382-20 (1-15) x CC062239 (1-517)

```

Qy 1 PheAlaValGluAnProMetAsnArgLeuValAlaGluThrLeu 15
|||||
Db 273 TTCAGTGGAAACCCGGTGAACCGTTGGTCTGCCAACCTT 317

```

RESULT 34

CZ331571

LOCUS

```

DEFINITION CZ331571 522 bp DNA linear GSS 24-MAR-2005
ZMBSF0039A12r ZMBSF Zea mays genomic clone ZMBSF0039A12 3', genomic
survey sequence.

```

ACCESSION

CZ331571

VERSION

CZ331571.1

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```

REFERENCE

AUTHORS

Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.

and Messing,J.

Construction, Sequencing and Characterization of a Posmid Library

of the B73 Maize Genome

Unpublished (2005)

CONTACT: Bharti,A.K.

Dr Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University

190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801

Fax: 732 445 5735

Email: bharti@waksman.rutgers.edu

Seq primer: Pos_R

Class: fosmid ends.

Features

source

1. .522

Location/Qualifiers

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="ZMBSF0039A12"

/lab_host="EPI100-T1"

/clone_lib="ZMBSF"

/note="Vector: pEpiFOS-5; Site_1: Eco72I"

ORIGIN

Alignment Scores:

```

Pred. No.: 401 Length: 522
Score: 43.00 Matches: 8
Percent Similarity: 78.57% Conservative: 3
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 58.11% Indels: 0
DB: 10 Gaps: 0

```

US-10-787-382-20 (1-15) x CZ331571 (1-522)

```

Qy 1 PheAlaValGluAnProMetAsnArgLeuValAlaGluThr 14
|||||
Db 131 TTTCGCTCATCTAATCCCTTGACCAAGCTAGTGAATCTACT 172

```

RESULT 35

CA877602

LOCUS

DEFINITION

CA877602

VERSION

CA877602.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Piao,Y., Dudekula,D.B., Qian,Y., Martin,P.R., Aiba,K., Vescovi,A.L.

and Ko,M.S.H.

Systematic Analyses of NIA Mouse Neural Stem Cell

(Undifferentiated) cDNA Library (long)

Unpublished (2002)

CONTACT: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: K0958 row: A column: 01

Seq primer: -21M13 Forward

High quality sequence stop: 536

POLYA=Yes.

Features

source

1. .536

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD1"

/db_xref="niaEST:K0958A01-3N"

/db_xref="taxon:10090"

/clone="NIA:K0958A01 IMAGE:30089760"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="NIA Mouse Neural Stem Cell (Undifferentiated)

cDNA Library (long)"

/note="Vector: pSPOR1 (Invitrogen); Site_1: SalI; Site_2:

NotI; Mouse cDNA project by the Laboratory of Genetics,

National Institute on Aging (NIA), Intramural Research

Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is

a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were

obtained from Dr. Angelo L. Vescovi (Institute for Stem

Cell Research, Italy). Double-stranded cDNAs were

synthesized with an Oligo(dT) primer [Invitrogen:

5'-PGACTAGTTCGAGCGCGCTTTT-3'] from

2.0 Microgram of total RNA, treated with T4 DNA

polymerase, and purified by ethanol-precipitation. The

cDNAs were ligated to Lone-linker IL-Sal4, purified by

phenol/chloroform, and separated from free linkers by

Centricon 100. Then, the cDNAs were amplified by

long-range high fidelity PCR using Ex Tag polymerase

(Takara) with a primer Sal4-S. The products were purified

by phenol/chloroform and Centricon 100. The cDNAs were

digested with SalI and NotI enzymes and cloned into

Sali/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 Kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:
Pred. No.: 414 Length: 536
Score: 43.00 Matches: 8
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 58.11% Indels: 0
DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x CA877602 (1-536)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAla 12
Db 364 TGGGCCCTTGAGATCTATTTCAGAGATTAGTTGCC 399

RESULT 36

CC578117

LOCUS CH240_456D24.TARBAC13P2 CHORI-240 Bos taurus genomic clone
DEFINITION CH240_456D24, genomic survey sequence.

ACCESSION CC578117.1 GI:31922460

VERSION GSS.

KEYWORDS Bos taurus (cow)

SOURCE Bos taurus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Holt, R., Scott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
Tsai, M., Cloutier, A., Lee, D., Ginn, N., Olson, T., Mayo, M.,
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
Schlein, J., Marra, M., de Jong, P., Keele, J.W. and Kappes, S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Other GSSs: CH240_456D24.T7

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rholt@bccgc.ca

Clones are derived from the bovine BAC library CHORI-240

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.

Plate: 456 row: D column: 24

Seq primer: SP6

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..553

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="Breed: Hereford"

/db_xref="taxon:9913"

/clone="CH240_456D24"

/sex="Male"

/cell_type="Blood"

/clone_lib="CHORI-240"

/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 429 Length: 553
Score: 43.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 58.11% Indels: 0
DB: 9 Gaps: 0

US-10-787-382-20 (1-15) x CC578117 (1-553)

Qy 1 PheAlaValGluAsnProMetAsnArg 9

Db 374 TTTGCCGTGGAGATCCCATGGACAGA 400

RESULT 37

CG841296

LOCUS Ynhw1910 HW-YUBAC Bos taurus genomic clone linear GSS 01-SEP-2004
DEFINITION 5', genomic survey sequence.

ACCESSION CG841296

VERSION CG841296.1 GI:51786324

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Choi, I.
Genomic sequences from Korean Cattle (Hanwoo) blood
Unpublished (2003)

JOURNAL

COMMENT

Molecular Biology

Yeungnam University

214-1, Dae-dong Gyeongsan, Korea 712-749

Tel: 82 53 810 2933

Fax: 82 53 816 3637

Email: inhchoi@yumail.ac.kr

Seq primer: T7 Forward

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..562

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="Korean Cattle (Hanwoo)"

/db_xref="taxon:9913"

/clone="HW-YUBAC2-184-1-D03-T7"

/sex="Male"

/tissue_type="Blood"

/cell_type="Leucocyte"

/dev_stage="Adult"

/clone_lib="HW-YUBAC"

/note="Vector: pIndigoBAC-5"

ORIGIN

Alignment Scores:
Pred. No.: 437 Length: 562
Score: 43.00 Matches: 8
Percent Similarity: 81.82% Conservative: 1
Best Local Similarity: 72.73% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x CG841296 (1-562)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuVal 11

Db 184 TTTTCCGTGGAGATCCCATGAACAGAGTC 216

RESULT 38

AZ759493

LOCUS AZ759493 591 bp DNA linear GSS 16-FEB-2001
 DEFINITION clone UUGC1M0552K03 F, genomic survey sequence.
 ACCESSION AZ759493
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 591)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0552 row: K column: 03
 Seq primer: CGTTGTAAACGACGCCGAGT
 Class: plasmid ends
 High quality sequence stop: 591.
 Location/Qualifiers
 1. 591
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0552K03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1. 591
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0552K03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
 Pred. No.: 463 Length: 591
 Score: 43.00 Matches: 8
 Percent Similarity: 75.00% Conservative: 1
 Best Local Similarity: 66.67% Mismatches: 3
 Query Match: 58.11% Indels: 0
 DB: 9 Gaps: 0

US-10-787-382-20 (1-15) x AZ759493 (1-591)

Qy
 Db
 RESULT 39
 CF799042
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

2 AlavalGluAenProMetAsnArgLeuValAlaGlu 13
 Lr_PAHCF_13B11_M13R Earthworm Fluorantene Exposure Library
 Lumbrius rubellus cDNA clone Lr_PAHCF_13B11 5', mRNA sequence.
 172 GCTGGGAGATCCATTCAATGAACAATAGCAGAA 207
 CF799042 598 bp mRNA linear EST 21-OCT-2003
 Lr_PAHCF_13B11_M13R Earthworm Fluorantene Exposure Library
 Lumbrius rubellus cDNA clone Lr_PAHCF_13B11 5', mRNA sequence.
 CF799042
 CF799042.1 GI:37803612
 EST.
 Lumbrius rubellus (humus earthworm)
 Lumbrius rubellus
 Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 Lumbicina; Lumbriidae; Lumbrius.
 1 (bases 1 to 598)
 Chaiseley, J., Hedley, B.A., Morgan, J.C., Sturzenbaum, S., Kille, P. and
 Blaxter, M.
 The Lumbrius rubellus EST program - Sequences from a Fluorantene
 Exposure library
 Unpublished (2003)
 Contact: Jennifer Chaiseley
 BIOSI 1
 Cardiff University
 Main College, Museum Avenue, Cardiff, CF11 3TL, UK
 Tel: +44 2920876680
 Fax: +44 2920874305
 Email: chaiseley@cardiff.ac.uk, Kille@cardiff.ac.uk
 Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
 library (Stratagene) protocol.
 PCR Primers
 FORWARD: gtttccacgtcacgacg
 BACKWARD: caggaacagctatgaccatg
 Plate: 13 row: B Column: 11
 Seq primer: caggaacagctatgaccatg
 High quality sequence stop: 496.
 Location/Qualifiers
 1. 598
 /organism="Lumbrius rubellus"
 /mol_type="mRNA"
 /db_xref="taxon:35632"
 /clone="Lr_PAHCF_13B11"
 /tissue_type="Whole worm"
 /dev_stage="Adult"
 /clone_lib="Earthworm Fluorantene Exposure Library"
 /note="Vector: pBluescript II SK+; The library was
 prepared using protocols given by the supplier
 (Stratagene)."

ORIGIN

Alignment Scores:
 Pred. No.: 469 Length: 598
 Score: 43.00 Matches: 8
 Percent Similarity: 91.67% Conservative: 3
 Best Local Similarity: 66.67% Mismatches: 1
 Query Match: 58.11% Indels: 0
 DB: 6 Gaps: 0

US-10-787-382-20 (1-15) x CF799042 (1-598)

Qy
 Db
 RESULT 40
 CG950325/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS

2 AlavalGluAenProMetAsnArgLeuValAlaGlu 13
 93 GCAGTGGAGAACCCGATGGACCGTGTGTGCTGGAT 128
 CG950325
 MBBFH66TF mth2 Medicago truncatula genomic clone 43L12, genomic
 survey sequence.
 CG950325
 CG950325.1 GI:39860697
 GSS.


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/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11464311"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
end-prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

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ORIGIN

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Alignment Scores:
Pred. No.: 506 Length: 639
Score: 43.00 Matches: 8
Percent Similarity: 90.91% Conservative: 2
Best Local Similarity: 72.73% Mismatches: 1
Query Match: 58.11% Indels: 0
DB: 10 Gaps: 0

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US-10-787-382-20 (1-15) x CW301651 (1-639)

QY 5 AsnProMetAenArgLeuValAlaGluThrLeu 15

DB 397 AACAACTAACAGGCTCATTGCAGAAACACTT 365

RESULT 43

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CW277572/2
LOCUS CW277572.1 665 bp DNA linear GSS 31-OCT-2004
DEFINITION 104 751_11406099_148 35413_004 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11406099, genomic survey
sequence.
ACCESSION CW277572
VERSION CW277572.1 GI:54993760
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 665)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McWenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 751 row: m column: 03
Seq primer: Swfor Forward
Class: methylation filtered
High quality sequence stop: 665.
Location/Qualifiers
1. .665
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11406099"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
end-prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector

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FEATURES

source

and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN

```

Alignment Scores:
Pred. No.: 530 Length: 665
Score: 43.00 Matches: 8
Percent Similarity: 90.91% Conservative: 2
Best Local Similarity: 72.73% Mismatches: 1
Query Match: 58.11% Indels: 0
DB: 10 Gaps: 0

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US-10-787-382-20 (1-15) x CW277572 (1-665)

QY 5 AsnProMetAenArgLeuValAlaGluThrLeu 15

DB 540 AACAACTAACAGGCTCATTGCAGAAACACTT 508

RESULT 44

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BB303483/3
LOCUS BB303483.2 678 bp mRNA linear EST 24-OCT-2001
DEFINITION BB303483 RIKEN full-length enriched, adult male corpora
Quadrigenina Mus musculus cDNA clone B230104L09 3', mRNA sequence.
ACCESSION BB303483
VERSION BB303483.2 GI:16402059
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 678)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,I., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 10, 2000 this sequence version replaced gi:9004188.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-5222
Fax: 81-45-503-5216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for

```



```

FEATURES
  source
    Class: BAC ends.
    Location/Qualifiers
      1. .682
        /organism="Trypanosoma cruzi"
        /mol_type="genomic DNA"
        /strain="CL Brener"
        /db_xref="taxon:5693"
        /clone="TC3-51G7"
        /clone_lib="TC3"
        /note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed
for Uppsala University by Marie-Christine Le Paslier in
the laboratory of Denis le Paslier at the Centre d'Etude
du Polymorphisme Humain (CEPH), Paris, France. Briefly,
Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained
from Dr. Franco da Silveira) was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBeloBAC11 digested with Hin dIII. The average insert
size is 100 kb. Total clone coverage: approx. 33 X the
haploid genome."
ORIGIN
Alignment Scores:
Pred. No.: 545 Length: 682
Score: 43.00 Matches: 7
Percent Similarity: 71.43% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 4
Query Match: 58.11% Indels: 0
DB: 9 Gaps: 0
US-10-787-382-20 (1-15) x BH845769 (1-682)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
Db 19 TTGTGTTGTGACGAGCCCAAAACAGAGTGATCACTGCACACC 60
RESULT 47
C2422877
LOCUS C2422877 683 bp DNA linear GSS 06-APR-2005
DEFINITION 1018580 RP42 Bos taurus genomic clone RP42-54G17, genomic survey
sequence.
ACCESSION C2422877
VERSION C2422877.1 GI:62310086
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 683)
Sonstegard,T.S., Van Tassel,C.P., Capuco,A.V., de Jong,P.,
Matukumalli,L.K., Shade,L.S., Bosak,S., Rubenfield,M. and
Gasbarre,L.C.
Bovine BAC End Sequences from Library RPCI-42
Unpublished (2005)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tad@anri.barc.uga.edu.gov
Clones are derived from the bovine BAC library RPCI-42
(http://bacpac.choi.org/mbovine42.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(http://www.choi.org/bacpac/ordering/information.html). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by USDA-ARS-BFGL.
Plate: 54 row: G column: 17
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends.
Location/Qualifiers
  1. .683
    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /strain="Holstein"
    /db_xref="taxon:9913"
    /clone="RP42-54G17"
    /sex="male"
    /cell_type="Blood"
    /clone_lib="RP42"
    /note="Vector: pBACe3.6; Site 1: MboI; Site 2: MboI;
RPCI-42 Bovine BAC library (Male Holstein) produced by
Pieter de Jong"
ORIGIN
Alignment Scores:
Pred. No.: 546 Length: 683
Score: 43.00 Matches: 7
Percent Similarity: 90.00% Conservative: 2
Best Local Similarity: 70.00% Mismatches: 1
Query Match: 58.11% Indels: 0
DB: 10 Gaps: 0
US-10-787-382-20 (1-15) x C2422877 (1-683)
Qy 1 PheAlaValGluAsnProMetAsnArgLeu 10
Db 382 TTTGCTCGAGAACCCCATGACAGGATG 411
RESULT 48
BB344850/c
LOCUS BB344850/c 708 bp mRNA linear EST 24-OCT-2001
DEFINITION BB344850 RIKEN full-length enriched, 10 days neonate cerebellum Mus
musculus cDNA clone B930053J07 3', mRNA sequence.
ACCESSION BB344850
VERSION BB344850.2 GI:16404903
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 708)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 12, 2000 this sequence version replaced gi:9054574.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wachiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.

```

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001) Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source
1. .708
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="B930053J07"
/sex="mixed"
/tissue_type="cerebellum"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 days neonate cerebellum"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGAGAGCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATAATTAATCCGCCGCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

ORIGIN

Alignment Scores:
Pred. No.: 569 Length: 708
Score: 43.00 Matches: 8
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 58.11% Indels: 0
DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x BB344850 (1-708)

QY 1 PheAlaValGluAsnProMetAsnArgLeuValAla 12
:::|||||:::|||||:::|||||:::|||||:::|||||
Db 350 TGGGCCCTTGAGATCTATTTCAGATTAGTTGCC 315

RESULT 49
AG170565/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-039J07.T7, genomic survey sequence.
ACCESSION AG170565
VERSION AG170565.1 GI:16700243
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Sequencing: T7
LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source

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/clone="RP43-039J07.T7"
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ORIGIN

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Percent Similarity: 90.91% Conservative: 3
Best Local Similarity: 63.64% Mismatches: 1
Query Match: 58.01% Indels: 0
DB: 10 Gaps: 0

US-10-787-382-20 (1-15) x AG170565 (1-720)

QY 3 ValGluAsnProMetAsnArgLeuValAlaGlu 13
:::|||||:::|||||:::|||||:::|||||
Db 457 ATAGAAACCCATTAAATAAACAGTAGCTGAA 425

RESULT 50

AG075393

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library RPCI-43

Unpublished

2 (bases 1 to 720)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: chimpesegsc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>,

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1. .720

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AG075393 722 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-068E13.F, genomic survey sequence.

AG075393

AG075393

AG075393.1 GI:16627195

GSS.

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Pan.

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 722)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbesc@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1..722

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ORIGIN

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US-10-787-382-20 (1-15) x AG075393 (1-722)

Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15

Db 385 GCAATTCAGAACCTCAGAACAGAAAAATATCAGAAACATTG 426

Search completed: December 21, 2005, 18:53:14

Job time : 2639 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 21, 2005, 16:41:26 ; Search time 138 Seconds
(without alignments)
193.213 Million cell updates/sec

Title: US-10-787-382-20
Perfect score: 74
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Fgapop 6.0, Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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C 130	37	50.0	1761	3	US-09-519-232-7	Sequence 7, Appl1	C 207	36	48.6	606	3	US-09-492-709A-232	Sequence 232, App
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C 132	37	50.0	2139	3	US-09-949-002-142	Sequence 142, App	C 209	36	48.6	624	3	US-10-178-213-46	Sequence 46, Appl
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C 134	37	50.0	2593	3	US-10-104-047-1010	Sequence 1010, Ap	C 211	36	48.6	657	3	US-09-248-796A-126	Sequence 126, App
C 135	37	50.0	2677	3	US-09-270-767-28385	Sequence 28385, A	C 212	36	48.6	700	3	US-09-735-271-470	Sequence 470, App
C 136	37	50.0	3106	3	US-09-323-872A-21	Sequence 21, Appl	C 213	36	48.6	700	3	US-09-735-271-471	Sequence 471, App
C 137	37	50.0	3106	3	US-09-072-433-13	Sequence 13, Appl	C 214	36	48.6	1047	3	US-09-221-017B-59	Sequence 59, Appl
C 138	37	50.0	3360	3	US-09-121-211-1	Sequence 1, Appl1	C 215	36	48.6	1239	3	US-09-894-844-68	Sequence 68, Appl
C 139	37	50.0	3420	2	US-08-117-491-25	Sequence 25, Appl	C 216	36	48.6	1266	3	US-09-533-559-5540	Sequence 5540, Ap
C 140	37	50.0	3420	2	US-08-271-364A-6	Sequence 6, Appl1	C 217	36	48.6	1266	3	US-09-489-039A-6230	Sequence 6230, Ap
C 141	37	50.0	3420	2	US-08-222-715B-25	Sequence 25, Appl	C 218	36	48.6	1266	3	US-09-581-148C-19	Sequence 19, Appl
C 142	37	50.0	4173	3	US-09-949-002-61	Sequence 61, Appl	C 219	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 143	37	50.0	4214	3	US-09-221-017B-293	Sequence 293, App	C 220	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 144	37	50.0	4320	3	US-09-134-000C-2728	Sequence 2728, Ap	C 221	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 145	37	50.0	4707	2	US-08-004-139B-2	Sequence 2, Appl1	C 222	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 146	37	50.0	4707	2	US-08-811-492-2	Sequence 2, Appl1	C 223	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 147	37	50.0	4928	3	PCT-US96-10545A-2	Sequence 2, Appl1	C 224	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 148	37	50.0	4928	3	US-09-323-872A-32	Sequence 32, Appl	C 225	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 149	37	50.0	4928	3	US-09-072-433-17	Sequence 17, Appl	C 226	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 150	37	50.0	5706	3	US-09-270-767-12590	Sequence 12590, A	C 227	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 151	37	50.0	6727	3	US-08-629-643A-5	Sequence 5, Appl1	C 228	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 152	37	50.0	6727	3	US-09-280-799-1	Sequence 1, Appl1	C 229	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 153	37	50.0	6727	3	US-09-155-884-5	Sequence 5, Appl1	C 230	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 154	37	50.0	9325	3	US-09-902-540-903	Sequence 903, App	C 231	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl
C 155	37	50.0	9482	3	US-09-949-016-14605	Sequence 14605, A	C 232	36	48.6	1507	2	US-07-906-871-13	Sequence 13, Appl

C 229	36	48.6	3255	2	US-08-717-515-5	Sequence 5, Appli	302	35	47.3	579	3	US-09-252-991A-15036	Sequence 15036, A
C 230	36	48.6	3279	6	PCT-US93-03077-2	Sequence 2, Appli	303	35	47.3	585	3	US-09-107-433-1045	Sequence 1045, Ap
C 231	36	48.6	3282	3	US-09-949-016-5664	Sequence 5664, Ap	304	35	47.3	594	3	US-09-902-540-7441	Sequence 7441, Ap
C 232	36	48.6	3831	2	US-08-717-515-7	Sequence 7, Appli	C 305	35	47.3	601	3	US-09-949-016-26797	Sequence 26797, A
C 233	36	48.6	4307	3	US-09-949-002-94	Sequence 94, Appli	C 306	35	47.3	601	3	US-09-949-016-28299	Sequence 28299, A
C 234	36	48.6	4407	3	US-10-012-231A-316	Sequence 316, App	C 307	35	47.3	601	3	US-09-949-016-28299	Sequence 28299, A
C 235	36	48.6	4407	3	US-10-013-389A-316	Sequence 316, App	C 308	35	47.3	601	3	US-09-949-016-33343	Sequence 33343, A
C 236	36	48.6	4407	3	US-10-006-768A-316	Sequence 316, App	C 309	35	47.3	601	3	US-09-949-016-33344	Sequence 33344, A
C 237	36	48.6	4407	3	US-10-015-671A-316	Sequence 316, App	C 310	35	47.3	601	3	US-09-949-016-68235	Sequence 68235, A
C 238	36	48.6	4407	3	US-10-015-393A-316	Sequence 316, App	C 311	35	47.3	601	3	US-09-949-016-159686	Sequence 159686, A
C 239	36	48.6	4407	3	US-10-011-833A-316	Sequence 316, App	C 312	35	47.3	601	3	US-09-949-016-169149	Sequence 169149, A
C 240	36	48.6	4407	3	US-10-006-041A-316	Sequence 316, App	C 313	35	47.3	601	3	US-09-949-016-171968	Sequence 171968, A
C 241	36	48.6	4407	3	US-10-012-064A-316	Sequence 316, App	C 314	35	47.3	601	3	US-09-949-016-182563	Sequence 182563, A
C 242	36	48.6	4562	3	US-09-620-312D-418	Sequence 418, App	C 315	35	47.3	601	3	US-09-949-016-182564	Sequence 182564, A
C 243	36	48.6	5495	2	US-08-602-010A-2	Sequence 1, Appli	C 316	35	47.3	601	3	US-09-949-016-182683	Sequence 182683, A
C 244	36	48.6	5495	2	US-08-602-010A-2	Sequence 2, Appli	C 317	35	47.3	601	3	US-09-949-016-182684	Sequence 182684, A
C 245	36	48.6	5495	2	US-08-680-726A-2	Sequence 1, Appli	C 318	35	47.3	601	3	US-09-949-016-188634	Sequence 188634, A
C 246	36	48.6	5495	2	US-08-680-726A-2	Sequence 2, Appli	C 319	35	47.3	601	3	US-09-949-016-188683	Sequence 188683, A
C 247	36	48.6	5495	3	US-09-092-409-1	Sequence 1, Appli	C 320	35	47.3	601	3	US-09-949-016-188732	Sequence 188732, A
C 248	36	48.6	5495	3	US-09-092-409-2	Sequence 2, Appli	C 321	35	47.3	601	3	US-09-949-016-188781	Sequence 188781, A
C 249	36	48.6	6294	3	US-08-976-259-5	Sequence 5, Appli	C 322	35	47.3	601	3	US-09-949-016-192865	Sequence 192865, A
C 250	36	48.6	6294	3	US-08-976-259-5	Sequence 5, Appli	C 323	35	47.3	601	3	US-09-949-016-192911	Sequence 192911, A
C 251	36	48.6	6830	2	US-08-822-445-1	Sequence 1, Appli	C 324	35	47.3	601	3	US-09-949-016-192957	Sequence 192957, A
C 252	36	48.6	6830	2	US-09-396-540-1	Sequence 1, Appli	C 325	35	47.3	601	3	US-09-949-016-193003	Sequence 193003, A
C 253	36	48.6	6866	3	US-09-949-016-15807	Sequence 15807, A	C 326	35	47.3	601	3	US-09-949-016-193049	Sequence 193049, A
C 254	36	48.6	10592	2	US-08-680-726A-51	Sequence 51, Appli	C 327	35	47.3	601	3	US-09-949-016-193142	Sequence 193142, A
C 255	36	48.6	10592	2	US-08-680-726A-52	Sequence 52, Appli	C 328	35	47.3	601	3	US-09-949-016-193235	Sequence 193235, A
C 256	36	48.6	10592	3	US-09-092-409-51	Sequence 51, Appli	C 329	35	47.3	601	3	US-09-949-016-193328	Sequence 193328, A
C 257	36	48.6	10592	3	US-09-092-409-52	Sequence 52, Appli	C 330	35	47.3	606	3	US-09-543-681A-3568	Sequence 3568, Ap
C 258	36	48.6	11073	3	US-09-949-016-15809	Sequence 15809, A	C 331	35	47.3	615	3	US-09-134-000C-674	Sequence 674, App
C 259	36	48.6	11165	3	US-09-830-807-34	Sequence 34, Appli	C 332	35	47.3	615	3	US-10-012-819-195	Sequence 195, App
C 260	36	48.6	12225	2	US-08-822-445-11	Sequence 11, Appli	C 333	35	47.3	648	3	US-09-543-681A-152	Sequence 152, App
C 261	36	48.6	12225	3	US-09-396-540-11	Sequence 11, Appli	C 334	35	47.3	745	3	US-09-107-532A-154	Sequence 154, App
C 262	36	48.6	12570	3	US-09-949-002-850	Sequence 850, App	C 335	35	47.3	745	3	US-08-858-207A-83	Sequence 83, Appli
C 263	36	48.6	12616	2	US-08-822-445-9	Sequence 9, Appli	C 336	35	47.3	768	3	US-09-252-991A-14591	Sequence 14591, A
C 264	36	48.6	16161	3	US-09-396-540-9	Sequence 9, Appli	C 337	35	47.3	777	3	US-09-252-991A-13903	Sequence 13903, A
C 265	36	48.6	20116	3	US-09-949-016-16861	Sequence 16861, A	C 338	35	47.3	777	3	US-09-252-991A-13903	Sequence 13903, A
C 266	36	48.6	20407	3	US-09-949-002-666	Sequence 666, App	C 339	35	47.3	780	3	US-09-489-039A-1590	Sequence 1590, Ap
C 267	36	48.6	32868	3	US-09-949-016-17406	Sequence 17406, A	C 340	35	47.3	828	3	US-09-489-039A-5862	Sequence 5862, Ap
C 268	36	48.6	47375	3	US-09-949-016-15420	Sequence 15420, A	C 341	35	47.3	849	3	US-09-107-433-842	Sequence 842, App
C 269	36	48.6	62311	3	US-09-949-016-14582	Sequence 14582, A	C 342	35	47.3	849	3	US-09-252-991A-15171	Sequence 15171, A
C 270	36	48.6	92304	3	US-09-949-016-15943	Sequence 15943, A	C 343	35	47.3	978	3	US-09-489-039A-2498	Sequence 2498, Ap
C 271	36	48.6	117391	3	US-09-949-016-13945	Sequence 13945, A	C 344	35	47.3	1080	3	US-09-248-736A-3766	Sequence 3766, Ap
C 272	36	48.6	126237	3	US-09-949-016-16674	Sequence 16674, A	C 345	35	47.3	1185	3	US-08-705-771-10	Sequence 10, Appli
C 273	36	48.6	126237	3	US-09-949-016-16675	Sequence 16675, A	C 346	35	47.3	1185	3	US-09-417-540-10	Sequence 10, Appli
C 274	36	48.6	168104	3	US-09-949-016-12026	Sequence 12026, A	C 347	35	47.3	1200	3	US-09-602-787A-465	Sequence 465, App
C 275	36	48.6	168105	3	US-09-949-016-15554	Sequence 15554, A	C 348	35	47.3	1278	3	US-09-252-991A-14456	Sequence 14456, A
C 276	36	48.6	198942	3	US-09-949-016-13209	Sequence 13209, A	C 349	35	47.3	1311	3	US-09-248-736A-3402	Sequence 3402, Ap
C 277	36	48.6	232024	3	US-09-949-016-13477	Sequence 13477, A	C 350	35	47.3	1314	3	US-09-902-540-8599	Sequence 8599, Ap
C 278	36	48.6	786431	3	US-09-751-389-3	Sequence 3, Appli	C 351	35	47.3	1344	3	US-09-583-110-1889	Sequence 1889, Ap
C 279	36	48.6	8403765	3	US-09-103-840A-2	Sequence 2, Appli	C 352	35	47.3	1368	3	US-09-540-236-405	Sequence 405, App
C 280	36	48.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli	C 353	35	47.3	1419	3	US-09-252-991A-13796	Sequence 13796, A
C 281	35	47.3	113	3	US-09-513-999C-33867	Sequence 33867, A	C 354	35	47.3	1583	3	US-09-620-312D-532	Sequence 532, App
C 282	35	47.3	228	3	US-09-107-433-766	Sequence 766, App	C 355	35	47.3	1599	3	US-09-902-540-7144	Sequence 7144, Ap
C 283	35	47.3	249	3	US-09-270-767-3988	Sequence 3988, Ap	C 356	35	47.3	1611	2	US-08-551-211-4	Sequence 4, Appli
C 284	35	47.3	249	3	US-09-270-767-13270	Sequence 13270, A	C 357	35	47.3	1771	3	US-09-270-767-13467	Sequence 13467, A
C 285	35	47.3	288	3	US-09-543-681A-3498	Sequence 3498, Ap	C 358	35	47.3	1773	3	US-09-495-797-40	Sequence 40, Appli
C 286	35	47.3	454	3	US-09-902-540-6951	Sequence 6951, Ap	C 359	35	47.3	1823	3	US-09-533-559-4781	Sequence 4781, Ap
C 287	35	47.3	456	3	US-09-489-039A-4007	Sequence 4007, Ap	C 360	35	47.3	1860	2	US-08-553-619B-1	Sequence 1, Appli
C 288	35	47.3	471	3	US-09-668-262A-5	Sequence 5, Appli	C 361	35	47.3	1866	3	US-09-668-262A-15	Sequence 15, Appli
C 289	35	47.3	493	3	US-09-702-705-750	Sequence 750, App	C 362	35	47.3	1866	3	US-10-427-442-15	Sequence 15, Appli
C 290	35	47.3	493	3	US-09-736-457-750	Sequence 750, App	C 363	35	47.3	1908	3	US-09-252-991A-14442	Sequence 14442, A
C 291	35	47.3	493	3	US-09-736-457-750	Sequence 750, App	C 364	35	47.3	1995	3	US-09-252-991A-13546	Sequence 13546, A
C 292	35	47.3	493	3	US-09-614-1248-750	Sequence 750, App	C 365	35	47.3	2010	3	US-09-527-972-3	Sequence 3, Appli
C 293	35	47.3	493	3	US-09-671-325-750	Sequence 750, App	C 366	35	47.3	2040	3	US-08-581-148C-21	Sequence 21, Appli
C 294	35	47.3	493	3	US-09-589-184-750	Sequence 750, App	C 367	35	47.3	2121	3	US-10-104-047-771	Sequence 771, App
C 295	35	47.3	493	3	US-09-658-824-750	Sequence 750, App	C 368	35	47.3	2202	2	US-08-551-211-5	Sequence 5, Appli
C 296	35	47.3	493	3	US-10-017-754-750	Sequence 750, App	C 369	35	47.3	2367	3	US-09-583-110-1278	Sequence 1278, Ap
C 297	35	47.3	493	3	US-09-651-563-750	Sequence 750, App	C 370	35	47.3	2539	3	US-08-581-148C-20	Sequence 20, Appli
C 298	35	47.3	522	3	US-09-519-642-750	Sequence 750, App	C 371	35	47.3	2571	3	US-09-107-433-931	Sequence 931, App
C 299	35	47.3	552	3	US-09-248-796A-2604	Sequence 2604, Ap	C 372	35	47.3	2621	2	US-08-553-619B-8	Sequence 8, Appli
C 300	35	47.3	552	3	US-09-621-976-190	Sequence 190, App	C 373	35	47.3	3215	3	US-09-155-885A-299	Sequence 299, App
C 301	35	47.3	558	3	US-09-583-110-2493	Sequence 2493, Ap	C 374	35	47.3	3446	3	US-09-620-312D-653	Sequence 653, App

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376	35	47.3	3559	3	US-08-472-285-1	Sequence 1, Appli	C 449	34	45.9	207	2	US-08-415-939-3	Sequence 3, Appli
377	35	47.3	3559	3	US-08-472-923-1	Sequence 1, Appli	C 450	34	45.9	293	3	US-09-313-294A-6389	Sequence 6389, Ap
378	35	47.3	3591	3	US-09-502-540-601	Sequence 601, App	C 451	34	45.9	332	3	US-09-270-767-31470	Sequence 31470, A
379	35	47.3	3599	3	US-09-902-540-655	Sequence 655, App	C 452	34	45.9	354	3	US-09-903-540-9128	Sequence 9128, Ap
380	35	47.3	4512	2	US-08-224-391-52	Sequence 52, Appl	C 453	34	45.9	414	3	US-09-270-767-28912	Sequence 28912, A
381	35	47.3	4512	2	US-08-484-304-52	Sequence 52, Appl	C 454	34	45.9	423	3	US-08-470-179-131	Sequence 131, App
382	35	47.3	5121	2	US-09-252-991A-15189	Sequence 15189, A	C 455	34	45.9	431	2	US-09-640-211A-491	Sequence 491, App
383	35	47.3	5173	2	US-08-242-677-1	Sequence 1, Appli	C 456	34	45.9	453	3	US-09-252-991A-12478	Sequence 12478, A
384	35	47.3	5432	3	US-09-214-139B-1	Sequence 1, Appli	C 457	34	45.9	468	2	US-08-324-003A-26	Sequence 26, Appl
385	35	47.3	5691	3	US-09-964-956-12	Sequence 12, Appl	C 458	34	45.9	468	2	US-09-755-836-26	Sequence 26, Appl
386	35	47.3	6327	3	US-09-252-991A-14931	Sequence 14931, A	C 459	34	45.9	480	2	US-08-324-003A-21	Sequence 21, Appl
387	35	47.3	6330	3	US-09-902-540-718	Sequence 718, App	C 460	34	45.9	480	2	US-09-755-836-21	Sequence 21, Appl
388	35	47.3	8703	3	US-08-961-527-177	Sequence 177, App	C 461	34	45.9	480	3	US-09-303-518D-355	Sequence 355, App
389	35	47.3	9412	2	US-08-955-138-1	Sequence 1, Appli	C 462	34	45.9	480	3	US-09-303-518D-357	Sequence 357, App
390	35	47.3	10236	3	US-09-949-016-1492	Sequence 12492, A	C 463	34	45.9	480	3	US-09-303-518D-363	Sequence 363, App
391	35	47.3	10237	3	US-09-949-016-13859	Sequence 13859, A	C 464	34	45.9	510	2	US-08-324-003A-16	Sequence 16, Appl
392	35	47.3	12128	3	US-09-949-016-12587	Sequence 12587, A	C 465	34	45.9	510	2	US-09-755-836-16	Sequence 16, Appl
393	35	47.3	12129	3	US-09-949-016-15713	Sequence 15713, A	C 466	34	45.9	513	2	US-09-252-991A-13628	Sequence 13628, A
394	35	47.3	13203	3	US-09-949-016-16606	Sequence 16606, A	C 467	34	45.9	525	2	US-08-324-003A-19	Sequence 19, Appl
395	35	47.3	14158	3	US-09-902-540-1069	Sequence 1069, Ap	C 468	34	45.9	525	3	US-09-755-836-13	Sequence 13, Appl
396	35	47.3	21296	3	US-09-949-016-14504	Sequence 14504, A	C 469	34	45.9	531	3	US-09-134-000C-816	Sequence 816, App
397	35	47.3	21296	3	US-09-949-016-14505	Sequence 14505, A	C 470	34	45.9	537	2	US-08-324-003A-24	Sequence 24, Appl
398	35	47.3	21296	3	US-09-949-016-15701	Sequence 15701, A	C 471	34	45.9	537	3	US-09-755-836-24	Sequence 24, Appl
399	35	47.3	21296	3	US-09-949-016-15702	Sequence 15702, A	C 472	34	45.9	543	3	US-09-253-991A-716	Sequence 716, App
400	35	47.3	28171	3	US-08-961-527-22	Sequence 22, Appl	C 473	34	45.9	549	3	US-09-583-110-1273	Sequence 1273, Ap
401	35	47.3	28194	3	US-09-902-540-1250	Sequence 1250, Ap	C 474	34	45.9	552	3	US-09-475-316A-98	Sequence 98, Appl
402	35	47.3	30365	3	US-09-825-414-1	Sequence 1, Appli	C 475	34	45.9	552	3	US-09-704-640-98	Sequence 98, Appl
403	35	47.3	31728	3	US-09-453-702B-64	Sequence 64, Appl	C 476	34	45.9	558	3	US-09-107-433-1932	Sequence 1932, Ap
404	35	47.3	31728	3	US-10-114-170-64	Sequence 64, Appl	C 477	34	45.9	574	2	US-08-905-267-8	Sequence 8, Appli
405	35	47.3	34017	3	US-09-949-016-17555	Sequence 17555, A	C 478	34	45.9	574	3	US-09-314-051-8	Sequence 8, Appli
406	35	47.3	46118	3	US-09-949-016-17003	Sequence 17003, A	C 479	34	45.9	574	3	US-09-617-389B-8	Sequence 8, Appli
407	35	47.3	47471	3	US-09-949-016-12271	Sequence 12271, A	C 480	34	45.9	595	3	US-09-533-559-1216	Sequence 1216, Ap
408	35	47.3	48682	3	US-09-949-016-17236	Sequence 17236, A	C 481	34	45.9	597	3	US-09-134-000C-894	Sequence 894, App
409	35	47.3	48682	3	US-09-949-016-17237	Sequence 17237, A	C 482	34	45.9	601	3	US-09-949-016-27373	Sequence 27373, A
410	35	47.3	48682	3	US-09-949-016-17238	Sequence 17238, A	C 483	34	45.9	601	3	US-09-949-016-27905	Sequence 27905, A
411	35	47.3	48682	3	US-09-949-016-17239	Sequence 17239, A	C 484	34	45.9	601	3	US-09-949-016-33935	Sequence 33935, A
412	35	47.3	51022	3	US-09-949-016-17135	Sequence 17135, A	C 485	34	45.9	601	3	US-09-949-016-35804	Sequence 35804, A
413	35	47.3	51022	3	US-09-949-016-17136	Sequence 17136, A	C 486	34	45.9	601	3	US-09-949-016-35882	Sequence 35882, A
414	35	47.3	51022	3	US-09-949-016-17137	Sequence 17137, A	C 487	34	45.9	601	3	US-09-949-016-35959	Sequence 35959, A
415	35	47.3	51022	3	US-09-949-016-17138	Sequence 17138, A	C 488	34	45.9	601	3	US-09-949-016-36046	Sequence 36046, A
416	35	47.3	55851	3	US-09-949-016-13732	Sequence 13732, A	C 489	34	45.9	601	3	US-09-949-016-38125	Sequence 38125, A
417	35	47.3	58385	3	US-09-949-016-14856	Sequence 14856, A	C 490	34	45.9	601	3	US-09-949-016-55282	Sequence 55282, A
418	35	47.3	78630	3	US-09-949-016-16790	Sequence 16790, A	C 491	34	45.9	601	3	US-09-949-016-62123	Sequence 62123, A
419	35	47.3	86213	3	US-09-949-016-17240	Sequence 17240, A	C 492	34	45.9	601	3	US-09-949-016-66305	Sequence 66305, A
420	35	47.3	86213	3	US-09-949-016-17241	Sequence 17241, A	C 493	34	45.9	601	3	US-09-949-016-68322	Sequence 68322, A
421	35	47.3	86213	3	US-09-949-016-17242	Sequence 17242, A	C 494	34	45.9	601	3	US-09-949-016-68756	Sequence 68756, A
422	35	47.3	86213	3	US-09-949-016-17243	Sequence 17243, A	C 495	34	45.9	601	3	US-09-949-016-71202	Sequence 71202, A
423	35	47.3	89450	3	US-09-949-016-15948	Sequence 15948, A	C 496	34	45.9	601	3	US-09-949-016-85008	Sequence 85008, A
424	35	47.3	92407	3	US-09-596-002-36	Sequence 36, Appl	C 497	34	45.9	601	3	US-09-949-016-85159	Sequence 85159, A
425	35	47.3	109038	3	US-09-949-016-12199	Sequence 12199, A	C 498	34	45.9	601	3	US-09-949-016-89153	Sequence 89153, A
426	35	47.3	113283	3	US-09-949-016-16976	Sequence 16976, A	C 499	34	45.9	601	3	US-09-949-016-127537	Sequence 127537, A
427	35	47.3	113283	3	US-09-949-016-16977	Sequence 16977, A	C 500	34	45.9	601	3	US-09-949-016-133063	Sequence 133063, A
428	35	47.3	115814	3	US-09-949-016-16205	Sequence 16205, A							
429	35	47.3	119649	3	US-09-949-016-12537	Sequence 12537, A							
430	35	47.3	137226	3	US-09-949-016-13763	Sequence 13763, A							
431	35	47.3	156324	3	US-09-949-016-13749	Sequence 13749, A							
432	35	47.3	168394	3	US-09-949-016-13002	Sequence 13002, A							
433	35	47.3	174639	3	US-09-949-016-16509	Sequence 16509, A							
434	35	47.3	181429	3	US-09-949-016-12372	Sequence 12372, A							
435	35	47.3	181430	3	US-09-949-016-15772	Sequence 15772, A							
436	35	47.3	221545	3	US-09-949-016-13875	Sequence 13875, A							
437	35	47.3	222552	3	US-09-949-016-12968	Sequence 12968, A							
438	35	47.3	227750	3	US-09-949-016-17175	Sequence 17175, A							
439	35	47.3	255679	3	US-09-949-016-17189	Sequence 17189, A							
440	35	47.3	536165	3	US-09-214-808-1	Sequence 1, Appli							
441	35	47.3	580073	3	US-08-545-528B-1	Sequence 1, Appli							
442	35	47.3	640691	3	US-09-790-988-1	Sequence 1, Appli							
443	34.5	46.6	1077	3	US-09-248-796A-3150	Sequence 3150, Ap							
444	34	45.9	202	2	US-09-513-999C-25816	Sequence 25816, A							
445	34	45.9	207	2	US-08-193-863-3	Sequence 3, Appli							
446	34	45.9	207	2	US-08-377-833-3	Sequence 3, Appli							
447	34	45.9	207	2	US-08-324-502-3	Sequence 3, Appli							

ALIGNMENTS

RESULT 1

US-09-322-409-85

; Sequence 85, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Ke

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-CI

; CURRENT APPLICATION NUMBER: US/09/322,409

; CURRENT FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85

Alignment Scores:
Pred. No.: 9.69e-07 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-85 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 45

RESULT 2

US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87

Alignment Scores:
Pred. No.: 9.69e-07 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-87 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 301

RESULT 3

US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Alignment Scores:
Pred. No.: 9.69e-07 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-85 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 45

RESULT 4

US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Alignment Scores:
Pred. No.: 9.69e-07 Length: 345
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-87 (1-345)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 301

```
RESULT 5
US-09-322-409-83
; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Alignment Scores:
Pred. No.: 1.18e-06 Length: 402
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-83 (1-402)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 58 TTTCGCTGAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 102

RESULT 6
US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84

Alignment Scores:
Pred. No.: 1.18e-06 Length: 402
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-84 (1-402)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
```

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Db 345 TTTCGCTGAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 301

RESULT 7
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83

Alignment Scores:
Pred. No.: 1.18e-06 Length: 402
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-83 (1-402)
QY 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 58 TTTCGCTGAGAAAATCCCATGAATAGACTGGTGGCAGACCTTG 102

RESULT 8
US-09-451-527-84/c
; Sequence 84, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

Alignment Scores:
Pred. No.: 1.18e-06 Length: 402
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-84 (1-402)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTG 301

RESULT 9

US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 036040017000500
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PstSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1

Alignment Scores:
Pred. No.: 1.19e-06 Length: 405
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-371-615A-1 (1-405)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTG 102

RESULT 10

US-09-322-409-80
; Sequence 80, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-80

Alignment Scores:
Pred. No.: 2.01e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-80 (1-610)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 86 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTG 130

RESULT 11

US-09-322-409-82/c
; Sequence 82, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-82

Alignment Scores:
Pred. No.: 2.01e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-322-409-82 (1-610)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 525 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTG 481

RESULT 12

US-09-451-527-80
; Sequence 80, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris

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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (29) ..(430)
US-09-451-527-80

Alignment Scores:
Pred. No.: 2,01e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-80 (1-610)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 86 TTTCGTGTAGAAAATCCCATGAATAGACTGGTGGCAGACACTTG 130

RESULT 13
US-09-451-527-82/c
/ Sequence 82, Application US/09451527
/ Patent No. 6482403
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ APPLICANT: Dreitz, Matthew J.
/ APPLICANT: Wonderling, Ramani S.
/ TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
/ FILE REFERENCE: IM-2-C2
/ CURRENT APPLICATION NUMBER: US/09/451,527
/ CURRENT FILING DATE: 1999-12-01
/ EARLIER APPLICATION NUMBER: 09/322,409
/ EARLIER FILING DATE: 1999-05-28
/ EARLIER APPLICATION NUMBER: 60/087,306
/ EARLIER FILING DATE: 1998-05-29
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 82
/ LENGTH: 610
/ TYPE: DNA
/ ORGANISM: Canis familiaris
US-09-451-527-82

Alignment Scores:
Pred. No.: 2,01e-06 Length: 610
Score: 74.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-451-527-82 (1-610)
Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 525 TTTCGTGTAGAAAATCCCATGAATAGACTGGTGGCAGACACTTG 481

RESULT 14
US-09-248-796A-8759
/ Sequence 8759, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstein et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409

/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ LENGTH: 210
/ TYPE: DNA
/ ORGANISM: Candida albicans
US-09-248-796A-8759

Alignment Scores:
Pred. No.: 2 Length: 210
Score: 43.00 Matches: 7
Percent Similarity: 90.91% Conservative: 3
Best Local Similarity: 63.64% Mismatches: 1
Query Match: 58.11% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-248-796A-8759 (1-210)
Qy 3 ValGluAsnProMetAsnArgLeuValAlaGlu 13
Db 73 ATTGAATTCCTTAACAGGTTGACAGCTAAA 105

RESULT 15
US-09-312-762A-3/c
/ Sequence 3, Application US/09312762A
/ Patent No. 6552177
/ GENERAL INFORMATION:
/ APPLICANT: MIA HOROWITZ ET AL.
/ TITLE OF INVENTION: EH DOMAIN CONTAINING GENES AND PROTEINS
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
/ STREET: 2001 Jefferson Davis Highway, Suite 207
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: United States of America
/ ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
/ COMPUTER: Twinhead* Slimnote-890TX
/ OPERATING SYSTEM: MS DOS version 6.2,
/ OPERATING SYSTEM: Windows version 3.11
/ SOFTWARE: Word for Windows version 2.0 converted to
/ SOFTWARE: an ASCII file
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/312,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/026,898
/ FILING DATE: 20 FEB 1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Friedmam, Mark M.
/ REGISTRATION NUMBER: 33,883
/ REFERENCE/DOCKET NUMBER: 916/10
/ TELEPHONE: 972-3-5625553
/ TELEFAX: 972-3-5625554
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14707
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
US-09-312-762A-3

Alignment Scores:
Pred. No.: 753 Length: 14707
Score: 42.00 Matches: 8
Percent Similarity: 69.23% Conservative: 1
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 56.76% Indels: 0
```

DB: 3 0 Gaps: 0
US-10-787-382-20 (1-15) x US-09-312-762A-3 (1-14707)
Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThr 14
Db 12589 GCTGCAGACATCTTCACGAGATTAAACAATGGAAACC 12551

RESULT 16

US-09-949-016-15393/c
; Sequence 15393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15393
; LENGTH: 194790
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15393

Alignment Scores:

Pred. No.:	2,06e+04	Length:	194790
Score:	42.00	Matches:	8
Percent Similarity:	81.82%	Conservative:	1
Best Local Similarity:	72.73%	Mismatches:	2
Query Match:	56.76%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-20 (1-15) x US-09-949-016-15393 (1-194790)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuVal 11

Db 29935 TTTCCTGAGATCCAGTTGGAAGATTGGTA 29903

RESULT 17

US-09-949-016-3240/c
; Sequence 3240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3240
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3240

Alignment Scores:

Pred. No.:	164	Length:	2085
Score:	40.00	Matches:	8
Percent Similarity:	69.23%	Conservative:	1
Best Local Similarity:	61.54%	Mismatches:	4
Query Match:	54.05%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-20 (1-15) x US-09-949-016-3240 (1-2085)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13

Db 2020 TTTCGCTAGAAAAGCCTTTTCAGAGTTGTTGAGGGAA 1982

RESULT 18

US-09-949-016-14982/c
; Sequence 14982, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14982
; LENGTH: 127771
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14982

Alignment Scores:

Pred. No.:	3,17e+04	Length:	127771
Score:	40.00	Matches:	8
Percent Similarity:	69.23%	Conservative:	1
Best Local Similarity:	61.54%	Mismatches:	4
Query Match:	54.05%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-20 (1-15) x US-09-949-016-14982 (1-127771)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGlu 13

Db 125705 TTTCGCTAGAAAAGCCTTTTCAGAGTTGTTGAGGGAA 125667

RESULT 19

US-09-949-016-14033/c
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14033
; LENGTH: 784019

```

; APPLICANT: TODARO, GEORGE J.
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
; FEATURE: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
; TITLE OF INVENTION: FIBROMATOSIS
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,326
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-680-326-23
;
; Alignment Scores:
; Pred. No.: 338 Length: 3027
; Score: 39.50 Matches: 10
; Percent Similarity: 66.67% Conservative: 0
; Best Local Similarity: 66.67% Mismatches: 2
; Query Match: 53.38% Indels: 3
; DB: 2 Gaps: 1
;
; US-10-787-382-20 (1-15) x US-08-680-326-23 (1-3027)
;
; Qy 3 ValGluAenPro-----MetAenArgLeuValAlaGluThr 14
; Db 731 GTGAGAACCCGTTGTCTATGATGAACCCGCTGGCGGCTCCACG 687
;
; RESULT 22
; US-08-434-001-138/c
; Sequence 138, Application US/08434001
; Patent No. 5712375
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; TITLE OF INVENTION: SELEX
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:

```



```

; APPLICATION NUMBER: US/08/433,585
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-433-585-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 51.67% Conservativeness: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 52.70% Indels: 0
DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x US-08-433-585-138 (1-71)

QY 4 GluAsnProMetAsnArgLeuValalaGluThrLeu 15
|||||:|||||:|||||:|||||:
Db 53 GAGAACCCCGTTCTCGCCTAGTCTCTCACAGTCTA 18

RESULT 24
US-08-434-425-138/c
; Sequence 138, Application US/08434425
; Patent No. 5789157
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,425
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131

```

```
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-434-425-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 52.70% Indels: 0
DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x US-08-434-425-138 (1-71)

QY 4 GluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 53 GAGAACCCGGTTCTCGCCTAGTCTCTCACAGTCTA 18

RESULT 25
US-08-437-667-138/c
; Sequence 138, Application US/08437667
; Patent No. 5864026
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,667
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-437-667-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 52.70% Indels: 0
DB: 2 Gaps: 0

US-10-787-382-20 (1-15) x US-08-437-667-138 (1-71)

QY 4 GluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 53 GAGAACCCGGTTCTCGCCTAGTCTCTCACAGTCTA 18

RESULT 26
US-08-906-955-138/c
; Sequence 138, Application US/08906955
; Patent No. 6013443
; GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-906-955-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-08-906-955-138 (1-71)
Qy 4 GluAenProMetAsnArgLeuValAlaGluThrLeu 15
Db 53 GAGAACCCCGTTCTCGCCTAGTCTCTCACAGTCTA 18

RESULT 27
US-08-905-909-138/c
; Sequence 138, Application US/08945909
; Patent No. 6114120
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
; TITLE OF INVENTION: ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,909
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06060
; FILING DATE: 01-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,425
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/437,667
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,585
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30C-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-909-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-08-945-909-138 (1-71)
Qy 4 GluAenProMetAsnArgLeuValAlaGluThrLeu 15
Db 53 GAGAACCCCGTTCTCGCCTAGTCTCTCACAGTCTA 18

RESULT 28
US-09-396-002A-138/c
; Sequence 138, Application US/09396002A
; Patent No. 6376474
; GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,002A
; FILING DATE: 14-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; APPLICATION NUMBER: 08/906,955
; FILING DATE: 05-AUGUST-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30-5/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 268-0066
; TELEFAX: (303) 268-0065
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-09-396-002A-138

Alignment Scores:
Pred. No.: 3.54 Length: 71
Score: 39.00 Matches: 7
Percent Similarity: 91.67% Conservative: 4
```



```

DB:                                     6           Gaps:                                0

US-10-787-382-20 (1-15) x PCT-US96-06060-138 (1-71)

Qy  4  GluAsnProMetAsnArgLeuValAlaGluThrLeu 15
      |||||:::|||||:::|||||:::|||||
Db   53  GAGAACCCGGTTCTCGCCTAGTCTCTACAGTCTA 18

RESULT 31
US-09-270-767-8641/c
; Sequence 8641, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8641
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8641

Alignment Scores:
Pred. No.:          45.6           Length:          523
Score:              39.00          Matches:         9
Percent Similarity: 66.67%         Conservative:    1
Best Local Similarity: 60.00%       Mismatches:     5
Query Match:        52.70%          Indels:         0
DB:                  3              Gaps:             0

US-10-787-382-20 (1-15) x US-09-270-767-8641 (1-523)

Qy  1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
      |||||:::|||||:::|||||:::|||||
Db   257  TTTCGGCTGGAGCGAGACCAGTACAAGCTGTGTGGCGGAGACCTG 213

RESULT 32
US-09-270-767-23923/c
; Sequence 23923, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23923
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23923

Alignment Scores:
Pred. No.:          45.6           Length:          523
Score:              39.00          Matches:         9
Percent Similarity: 66.67%         Conservative:    1
Best Local Similarity: 60.00%       Mismatches:     5
Query Match:        52.70%          Indels:         0
DB:                  3              Gaps:             0

US-10-787-382-20 (1-15) x US-09-270-767-23923 (1-523)

Qy  1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
      |||||:::|||||:::|||||:::|||||
Db   257  TTTCGGCTGGAGCGAGACCAGTACAAGCTGTGTGGCGGAGACCTG 213

RESULT 33

```

```

US-09-949-016-45191/c
; Sequence 45191, Application US/09949016
; Patent No. 6812139
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45191
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45191

Alignment Scores:
Pred. NO.: 54.5 Length: 601
Score: 39.00 Matches: 8
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 53.33% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-949-016-45191 (1-601)

Qy 1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 552 TTTCCCGTATCCAACTCTCATGACAGGATTGTGAGGGAGATATTA 508

RESULT 34
US-09-222-575-86
; Sequence 86, Application US/09222575
; Patent No. 6387897
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-86

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-222-575-86 (1-806)

Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
Db 100 GCCTTGGAAACCCCAAAACAGGACTGTGTGCAACTGTG 141

```

```
RESULT 35
US-09-389-681-72
; Sequence 72, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-72

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-389-681-72 (1-806)
QY 2 AlavalGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||:||||| ||| ||||| ||||| |||||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGACAACTCTG 141

RESULT 36
US-09-389-681-86
; Sequence 86, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-86

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-389-681-86 (1-806)
QY 2 AlavalGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||:||||| ||| ||||| ||||| |||||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGACAACTCTG 141
```

```
RESULT 37
US-09-620-405B-72
; Sequence 72, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-72

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-620-405B-72 (1-806)
QY 2 AlavalGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||:||||| ||| ||||| ||||| |||||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGACAACTCTG 141

RESULT 38
US-09-620-405B-86
; Sequence 86, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-86

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0

US-10-787-382-20 (1-15) x US-09-620-405B-86 (1-806)
QY 2 AlavalGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
|||:||||| ||| ||||| ||||| |||||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGACAACTCTG 141
```

```
Db      100 GCCTTGGAAAAACCCCAAAACAGGAGCTGTGTGTGACAACTCTG 141
||||:||||| ||| |||||| ||| |||||
RESULT 39
US-09-339-338-72
; Sequence 72, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-72

Alignment Scores:
Pred. No.:      79.4      Length:      806
Score:          39.00     Matches:      8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match:    52.70%   Indels:      0
DB:             3        Gaps:       0

US-10-787-382-20 (1-15) x US-09-339-338-72 (1-806)

Qy      2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| |||||| ||| |||||
Db      100 GCCTTGGAAAAACCCCAAAACAGGAGCTGTGTGTGACAACTCTG 141
||||:||||| ||| |||||| ||| |||||
RESULT 40
US-09-339-338-86
; Sequence 86, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-86

Alignment Scores:
Pred. No.:      79.4      Length:      806
Score:          39.00     Matches:      8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match:    52.70%   Indels:      0
DB:             3        Gaps:       0

US-10-787-382-20 (1-15) x US-09-339-338-86 (1-806)

Qy      2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| |||||| ||| |||||
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```
Db      100 GCCTTGGAAAAACCCCAAAACAGGAGCTGTGTGTGACAACTCTG 141
||||:||||| ||| |||||| ||| |||||
RESULT 41
US-09-433-826B-72
; Sequence 72, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-72

Alignment Scores:
Pred. No.:      79.4      Length:      806
Score:          39.00     Matches:      8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match:    52.70%   Indels:      0
DB:             3        Gaps:       0

US-10-787-382-20 (1-15) x US-09-433-826B-72 (1-806)

Qy      2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| |||||| ||| |||||
Db      100 GCCTTGGAAAAACCCCAAAACAGGAGCTGTGTGTGACAACTCTG 141
||||:||||| ||| |||||| ||| |||||
RESULT 42
US-09-433-826B-86
; Sequence 86, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-86

Alignment Scores:
Pred. No.:      79.4      Length:      806
Score:          39.00     Matches:      8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match:    52.70%   Indels:      0
DB:             3        Gaps:       0

US-10-787-382-20 (1-15) x US-09-433-826B-86 (1-806)

Qy      2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| |||||| ||| |||||
```

```
Db 100 GCCTTGGAAACCCCAACAGGACTGTGTGACAACTCTG 141
||||:||||| ||| ||||| ||| |||||
US-09-604-287A-72
RESULT 43
; Sequence 72, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-72
Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-20 (1-15) x US-09-604-287A-72 (1-806)
QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| ||| |||||
Db 100 GCCTTGGAAACCCCAACAGGACTGTGTGACAACTCTG 141
||||:||||| ||| ||||| ||| |||||
US-09-604-287A-86
RESULT 44
; Sequence 86, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-86
Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-20 (1-15) x US-09-604-287A-86 (1-806)
```

```
US-10-787-382-20 (1-15) x US-09-604-287A-86 (1-806)
QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| ||| |||||
Db 100 GCCTTGGAAACCCCAACAGGACTGTGTGACAACTCTG 141
||||:||||| ||| ||||| ||| |||||
US-09-285-480-72
RESULT 45
; Sequence 72, Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C1
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-285-480-72
Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-20 (1-15) x US-09-285-480-72 (1-806)
QY 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| ||| |||||
Db 100 GCCTTGGAAACCCCAACAGGACTGTGTGACAACTCTG 141
||||:||||| ||| ||||| ||| |||||
US-09-285-480-86
RESULT 46
; Sequence 86, Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C1
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-285-480-86
Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
DB: 3 Gaps: 0
US-10-787-382-20 (1-15) x US-09-285-480-86 (1-806)
```



```
Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| |||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGTGACAACTCTG 141

RESULT 47
US-09-834-759-72
; Sequence 72, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-72

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
Gaps: 0
Db:

US-10-787-382-20 (1-15) x US-09-834-759-72 (1-806)
Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| |||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGTGACAACTCTG 141

RESULT 48
US-09-834-759-86
; Sequence 86, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-86

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
Gaps: 0
Db:

US-10-787-382-20 (1-15) x US-09-834-759-86 (1-806)
Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| |||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGTGACAACTCTG 141

RESULT 49
US-09-590-751A-72
; Sequence 72, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-751A-72

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
Gaps: 0
Db:

US-10-787-382-20 (1-15) x US-09-590-751A-72 (1-806)
Qy 2 AlaValGluAenProMetAsnArgLeuValAlaGluThrLeu 15
||||:||||| ||| ||||| |||
Db 100 GCCTTGGAAAAACCCCAAAACAGGACTGTGTGTGACAACTCTG 141

RESULT 50
US-09-590-751A-86
; Sequence 86, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-751A-86

Alignment Scores:
Pred. No.: 79.4 Length: 806
Score: 39.00 Matches: 8
Percent Similarity: 64.29% Conservative: 1
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 52.70% Indels: 0
Gaps: 0
Db:
```

Percent Similarity:	64.29%	Conservative:	1
Best Local Similarity:	57.14%	Mismatches:	5
Query Match:	52.70%	Indels:	0
DB:	3	Gaps:	0

US-10-787-382-20 (1-15) x US-09-590-751A-86 (1-806)

Qy 2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeu 15

Db 100 GCCTTGGAACCCCAACAGGACTGTGTGACAACTCTG 141

Search completed: December 21, 2005, 18:10:02
 Job time : 192 secs